

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:24:02 ; Search time 17 Seconds
(without alignments)
1537.601 Million cell updates/sec

Title: US-09-703-951A-12
Perfect score: 2702
Sequence: 1 MRCSPGGVWLALASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2702	100.0	502	1 ACH7 HUMAN	P36544 homo sapien
2	2549	94.3	502	1 ACH7 MOUSE	P49582 mus musculus
3	2540	94.0	502	1 ACH7 BOVIN	P54131 bos taurus
4	2535	93.8	502	1 ACH7 RAT	P05941 rattus norv
5	2433	90.0	502	1 ACH7 CHICK	P22770 gallus gall
6	1108.5	41.0	498	1 ACH1 CAEEL	P48180 caenorhabdi
7	964.5	35.7	516	1 ACH1 WANSE	P91766 manduca sex
8	949	35.1	529	1 ACH2 HUMAN	Q15822 homo sapien
9	949	35.1	557	1 ACH1 SCHGR	P23414 schistocerc
10	944.5	35.0	511	1 ACH2 RAT	P12389 rattus norv
11	942.5	34.9	459	1 ACHN CARAU	P19370 carassius a
12	941.5	34.8	528	1 ACH2 CHICK	P09480 gallus gall
13	938	34.7	622	1 ACH4 CHICK	P09482 gallus gall
14	937.5	34.7	576	1 ACH2 DROME	P17644 drosophila
15	936	34.6	503	1 ACH3 HUMAN	P32297 homo sapien
16	926	34.3	496	1 ACH3 CHICK	P09481 gallus gall
17	926	34.3	567	1 ACH1 DROME	P09478 drosophila
18	923	34.2	629	1 ACH4 MOUSE	O70174 mus musculus
19	920	34.0	627	1 ACH4 HUMAN	P43681 homo sapien
20	919.5	34.0	495	1 ACH3 BOVIN	Q07263 bos taurus
21	914	33.8	495	1 ACHP RAT	P12392 rattus norv
22	912	33.8	630	1 ACH4 RAT	P09483 rattus norv
23	905.5	33.5	499	1 ACH3 RAT	P04757 rattus norv
24	898	32.9	494	1 ACH6 CHICK	P49581 gallus gall
25	885	32.8	498	1 ACHP HUMAN	P30926 homo sapien
26	882	32.6	521	1 ACH3 DROME	P04755 drosophila
27	880.5	32.6	491	1 ACHN CHICK	P09484 gallus gall
28	880	32.6	470	1 ACHP CHICK	P26153 gallus gall
29	878	32.5	512	1 ACH3 CARAU	P18945 carassius a
30	871.5	32.3	450	1 ACHX HUMAN	Q9GZ26 homo sapien
31	871.5	32.3	494	1 ACH6 HUMAN	Q15825 homo sapien
32	866.5	32.1	493	1 ACH6 RAT	P43143 rattus norv
33	865	32.0	502	1 ACHN HUMAN	P17787 homo sapien

RESULT 1

ACH7 HUMAN

ID ACH7 HUMAN STANDARD; PRT; 502 AA.

AC P36544; Q15826; Q96RH2; Q99555; Q9BXH0;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.

GN CHRNA7 OR NACHRA7.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

EX MEDLINE=94195283; PubMed=8145738;

RA Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;

RT "Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SY5Y cell line and determination of pharmacological

properties of native receptors and functional alpha 7 homomers

RT expressed in Xenopus oocytes.";

RL Mol. Pharmacol. 45:546-554(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Hippocampus;

RA Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;

RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RL MEDLINE=97062879; PubMed=8906617;

RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,

Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;

RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta

2-beta 4 nicotinic acetylcholine receptor subunits and functional

expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and

beta 4 subunits.";

RL J. Mol. Neurosci. 7:217-228(1996).

RN [4]

RP SEQUENCE FROM N.A.

RL MEDLINE=97162233; PubMed=9009220;

RA Groot Kormelink P.J., Luyten W.H.M.L.;

RT "Cloning and sequence of full-length cDNAs encoding the human neuronal

nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and

expression of seven nAChR subunits in the human neuroblastoma cell

line SH-SY5Y and/or IMR-32.";

RL FEBS Lett. 400:309-314(1997).

RN [5]

RP REVISIONS.

RA Groot Kormelink P.J., Luyten W.H.M.L.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RC TISSUE=Epidermal keratinocytes;

RA Arredondo J., Grando S.A.;

RT "Cloning cholinergic receptors in human keratinocytes.";

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [7]
 RN SEQUENCE OF 17-502 FROM N.A.
 RC TISSUE=Brain;
 RA Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
 RA Lee J., Tian J., Giordano T.;
 RT "Cloning and sequence of the human $\alpha 7$ nicotinic acetylcholine
 RT receptor";
 RL Drug Dev. Res. 30:252-256 (1993).
 RN [8]
 RN SEQUENCE OF 24-502 FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=94245214; PubMed=8188270;
 RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretto M.,
 RA Heinemann S.F.;
 RT "Molecular cloning and chromosomal localization of the human $\alpha 7$ -
 RT nicotinic receptor subunit gene (CHRNA7).";
 RL Genomics 19:379-381 (1994).
 RN [9]
 RN SEQUENCE OF 118-129 FROM N.A.
 RX MEDLINE=21818878; PubMed=11829490;
 RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
 RT "A 3-Mb map of a large segmental duplication overlapping the $\alpha 7$ -
 RT nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14";
 RL Genomics 79:197-209 (2002).
 RN [10]
 RN MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 RT protein expression map database";
 RL Proteomics 2:212-223 (2002).
 CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
 CC extensive change in conformation that affects all subunits and
 CC leads to opening of an ion-conducting channel across the plasma
 CC membrane.
 CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
 CC bungarotoxin. The structure is probably pentameric (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- MASS SPECTROMETRY: MW=54157.68; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
 CC -----
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 CC -----
 CC EMBL; X70297; CAA49778.1; -;
 DR EMBL; U40583; AAB3561.1; -;
 DR EMBL; Y02436; AAB40114.1; -;
 DR EMBL; Y08420; CAA69697.1; -;
 DR EMBL; AF385585; AAK68111.1; -;
 DR EMBL; L25827; -; NOT ANNOTATED_CDS.
 DR EMBL; Z23141; CAA80872.1; -;
 DR EMBL; AF332758; AAK19515.1; -;
 DR PIR; G02259; G02259.
 DR PIR; I37185; ACHUA7.
 DR Genew; HGNC:1960; CHRNA7.
 DR MIM; 118511; -;
 DR GO; GO:000592; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.
 DR GO; GO:0015464; F:acetylcholine receptor activity; TAS.
 DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. .; TAS.
 DR GO; GO:0000187; P:activation of MAPK; TAS.
 DR GO; GO:0006810; P:transport; TAS.
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neu_chan_LBD.

DR InterPro; IPR006201; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 22
 FT CHAIN 23 502
 FT BY SIMILARITY
 FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT POTENTIAL.
 FT BY SIMILARITY.
 FT ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT A -> G (IN REF. 1 AND 7).
 FT S -> N (IN REF. 2 AND 6).
 FT S -> P (IN REF. 2 AND 6).
 FT C -> S (IN REF. 8).
 FT A -> G (IN REF. 1).
 FT RMACS -> AWPAP (IN REF. 8).
 FT CONFLICT 409 413
 FT CONSEQUENCE 502 AA; 56449 MW; D94B3A482EAA0E42 CRC64;
 SQ
 Query Match 100.0%; Score 2702; DB 1; Length 502;
 Best Local Similarity 100.0%; Pred. No. 9.6e-213;
 Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MRCPGCVWALAAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQELTVYFSL 60
 Db 1 MRCPGCVWALAAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQELTVYFSL 60
 Qy 61 QIMDVDEKNOVLTNTIWLQMSWDHYLQWNVSEYGVKTVRFPDQGLWKPDILLYNSADE 120
 Db 61 QIMDVDEKNOVLTNTIWLQMSWDHYLQWNVSEYGVKTVRFPDQGLWKPDILLYNSADE 120
 Qy 121 RFDATEFTNVLNVSSGHGHCQLPPGIPKSSCYIDVRWFPFVQHCXKLFSGWSYGSW 180
 Db 121 RFDATEFTNVLNVSSGHGHCQLPPGIPKSSCYIDVRWFPFVQHCXKLFSGWSYGSW 180
 Qy 181 QMQEADISGYIPNGENDLVGIPGKRSEPFYECCKEYPDVTFTVMRRRLYYGLNLLIP 240
 Db 181 QMQEADISGYIPNGENDLVGIPGKRSEPFYECCKEYPDVTFTVMRRRLYYGLNLLIP 240
 Qy 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLTAQYFAS 300
 Db 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLTAQYFAS 300
 Qy 301 MIIVGLSVVTVTVLQYHHHDPDGGKMPKWKTRVILLNWCWFLRMKRPGEKVRPAQCHK 360
 Db 301 MIIVGLSVVTVTVLQYHHHDPDGGKMPKWKTRVILLNWCWFLRMKRPGEKVRPAQCHK 360
 Qy 361 QRRCSLASVEMSAVAPPPASNGMLLYIGFRLGDLGHCVCPTPDGSGVCGRMACSFTHDEHL 420
 Db 361 QRRCSLASVEMSAVAPPPASNGMLLYIGFRLGDLGHCVCPTPDGSGVCGRMACSFTHDEHL 420
 Qy 421 LHGGQPPGPDPLAKILEEVRYIANFRCCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPPGPDPLAKILEEVRYIANFRCCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

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ACH7 MOUSE
ID ACH7 MOUSE STANDARD; PRT; 502 AA.
AC P49582;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR ACH7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=95324936; PubMed=7601470;
RA Orr-Urtreger A., Seidlin M.F., Baldini A., Beaudet A.L.;
RT "Cloning and mapping of the mouse alpha 7-neuronal nicotinic
RT acetylcholine receptor."
RL Genomics 26:399-402(1995).
CC -!- FUNCTION: After binding acetylcholine, the ACHR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
CC bungarotoxin. The structure is probably pentameric (By
CC similarity).
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; L37663; AAC42053.1; -
CC PIR; A57175; A57175.
CC MGI; MGI:99779; Chrna7.
CC InterPro; IPR006029; Neu channel memb.
CC InterPro; IPR006202; Neu_chan_LBD.
CC InterPro; IPR006201; Neu channel.
CC Pfam; PF02931; Neur chan_LBD; 1.
CC Pfam; PF02932; Neur chan memb; 1.
CC PRINTS; PR00252; NRIONCHANNEL.
CC TIGRFAMs; TIGR00860; LIC; 1.
CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
CC Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 502
FT BY SIMILARITY.
FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT ALPHA-7 CHAIN. (POTENTIAL).
FT DOMAIN 23 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT DOMAIN 318 469
FT TRANSMEM 470 490
FT DISULFID 150 164
FT DISULFID 212 213
FT BY SIMILARITY.
FT ASSOCIATED WITH RECEPTOR ACTIVATION
FT (BY SIMILARITY).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 502 AA; 56631 MW; C9312E5226D120E3 CRC64;
Query Match 94.3%; Score 2549; DB 1; Length 502;
Best Local Similarity 94.0%; Pred. No. 2.9e-200;
Matches 467; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

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QY

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6 GGIMLALAAALLHVSLSQGEFORLYKELVKNYNPLERPVANDSQPLTVYFSLSLIQIMDV 65
Db
66 DEKNQVLTNTINWLSQMTDHYLQNVSEYPCGKTVRPDGOIKWPKDILLNLSADERPDAT 125
QY
66 DEKNQVLTNTINWLSQMTDHYLQNVSEYPCGKTVRPDGOIKWPKDILLNLSADERPDAT 125
Db
126 FHTNVLNNSGHCQYLPPGIPKSSCYIDVRWFPPDVQCKLKFGSWSYGWSLDMQGEA 185
QY
126 FHTNVLNNSGHCQYLPPGIPKSSCYIDVRWFPPDVQCKLKFGSWSYGWSLDMQGEA 185
Db
186 DISGIYNGEWDLVGIPKRSERYECCKEYPDVTFTVTRRTLYYGLNLLPCVLIS 245
QY
186 DISSYIIPNGEWDLVGIPKRSERYECCKEYPDVTFTVTRRTLYYGLNLLPCVLIS 245
Db
246 ALALLVLLPADSGEKISLGITVLLSLTVFMLVAETMPATSDSVPLIAQFAFSTMIIVG 305
QY
246 ALALLVLLPADSGEKISLGITVLLSLTVFMLVAETMPATSDSVPLIAQFAFSTMIIVG 305
Db
306 LSVVTVTVIQLYHHDPDGGKMPKWTIRVILLNWCANFLRMKRPGEKVRPAQCHKPRCS 365
QY
306 LSVVTVTVIQLYHHDPDGGKMPKWTIRVILLNWCANFLRMKRPGEKVRPAQCHKPRCS 365
Db
366 LASVEMSAVAPPASNGNLLYIGRGLDVHCVPTDPSGVVCGRMACSPTHDEHLHGGQ 425
QY
366 LASVELSAGAPPTSGNLLYIGRGLGEMHCAPTDPDSGVVCGRLACSPTHDEHLHGGH 425
Db
426 PPEGDPDLAKLLEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFVFTICTIG 485
QY
426 PDSGDPDLAKLLEEVRYIANFRQDESEVCSWKFAACVVDRLCLMAFVFTICTIG 485
Db
486 ILMSAPNFVEAVSKDFA 502
QY
486 ILMSAPNFVEAVSKDFA 502
Db

RESULT 3
ACH7 BOVIN
ID ACH7 BOVIN STANDARD; PRT; 499 AA.
AC P54131;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Adrenal medulla;
RX MEDLINE=95346009; PubMed=7620615;
RA Garcia-Guzman M.; Sala F., Sala S., Campos-Caro A., Stuehmer W.,
RA Gutierrez L., Criado M.;
RT "Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine
RT chromaffin cells: molecular cloning, functional expression and
RT alternative splicing of the alpha 7 subunit.";
RL Eur. J. Neurosci. 7:647-655(1995).
CC -!- FUNCTION: After binding acetylcholine, the ACHR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
CC bungarotoxin. The structure is probably pentameric (By
CC similarity). Homo-oligomer of the short form gives rise to
CC unfunctional channels, as does coexpression of both long and short
CC forms of the receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;

```

QY 6 GGIMLALAAALLHVSLSQGEFORLYKELVKNYNPLERPVANDSQPLTVYFSLSLIQIMDV 65

```
CC      IsoId=PS4131-1; Sequence=Displayed;
CC      Name=Short;
CC      IsoId=PS4131-2; Sequence=VSP_000075;
CC      TISSUE SPECIFICITY: At least in chromaffin cells.
CC      -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC      -----
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CC      -----
CC      EMBL: X93604; CAA63802.1; -
CC      InterPro: IPR006029; Neu_channel memb.
CC      InterPro: IPR006202; Neur_chan_LBD.
CC      InterPro: IPR006201; Neur_chan_LBD.
CC      Pfam: PF02931; Neur_chan_LBD; 1.
CC      Pfam: PF02932; Neur_chan memb; 1.
CC      PRINTS: PR00252; NRIONCHANNEL.
CC      TIGRFS: TIGR00860; LIC; 1.
CC      PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
CC      Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
CC      Transmembrane; Multigene family; Alternative splicing.
CC      SIGNAL 1 19
CC      CHAIN 20 499
CC      NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
CC      ALPHA-7 CHAIN.
CC      DOMAIN 20 227
CC      EXTRACELLULAR (POTENTIAL).
CC      TRANSMEM 228 252
CC      POTENTIAL.
CC      TRANSMEM 259 277
CC      POTENTIAL.
CC      TRANSMEM 293 314
CC      POTENTIAL.
CC      DOMAIN 315 466
CC      CYTOPLASMIC (POTENTIAL).
CC      TRANSMEM 467 487
CC      POTENTIAL.
CC      DISULFID 147 161
CC      BY SIMILARITY.
CC      ASSOCIATED WITH RECEPTOR ACTIVATION
CC      (BY SIMILARITY).
CC      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      Missing (in isoform Short).
CC      /FTID=VSP_000075.
CC      SEQUENCE 499 AA; 56002 MW; AEE5D0B382D042D5 CRC64;
Query Match 94.0%; Score 2540; DB 1; Length 499;
Best Local Similarity 94.6%; Pred. No. 1.6e-199;
Matches 470; Conservative 15; Mismatches 12; Indels 0; Gaps 0;
QY 6 GGVNLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSPLTVYFSLSLQIMDV 65
DB 3 GSLCLALAASLLHVSLOGEFQKLYKOLVKNYNPLERPVANDSPLTVYFSLSLQIMDV 62
QY 66 DEKNQVLTNTLWQMSWDHVLQNVSEYGVKTVRPDGOIWKPDILLYNSADERFAT 125
DB 63 DEKNQVLTNTLWQMTDHLQNVASBPYGVKTVRPDGOIWKPDILLYNSADERFAT 122
QY 126 FHTNVLNNSGHCQVLPFGIKSSCYIDVRFPFDVQCKLKFGSWSYGGSLDLQMQEA 185
DB 123 FHTNVLNNSGHCQVLPFGIKSSCYIDVRFPFDVQCKLKFGSWSYGGSLDLQMQEA 182
QY 186 DISGYPNGEWDLVGIPKGRSEFVECKEYPDVTFTVMRRRTLYGLMLLIPCVLIS 245
DB 183 DISGYPNGEWDLVGVLGKRSEKFECKEYPDVTFTVMRRRTLYGLMLLIPCVLIS 242
QY 246 ALALVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPFLIAQVFASTMIIVG 305
DB 243 ALALVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPFLIAQVFASTMIIVG 302
QY 306 LSVVVTIVLVQYHHHDPOGKMPKTRVILLNWCWAFLEMRKPGEDKVRPACQHKQRCS 365
DB 303 LSVVVTIVLVQYHHHDPOGKMPKTRVILLNWCWAFLEMRKPGEDKVRPACQHKQRCS 362
QY 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHLLHGGQ 425
```

```
DB 363 LASVEMSAVAPPATNGNLLYIGFRGLDTMHCAPTDPDSGVVCGRVACSTPHDEHLLHAGQ 422
QY 426 PREGPDDIAKILIEEYRYTANRERCODESAVCSSEKFAACVVDRLCLMAFSVFTICTIG 485
DB 423 PREGPDDIAKILIEEYRYTANRERCODESAVCSSEKFAACVVDRLCLMAFSVFTICTIG 482
QY 486 ILMSAPNFVEAVSKDFA 502
DB 483 ILMSAPNFVEAVSKDFA 499
RESULT 4
ID ACH7 RAT STANDARD; PRT; 502 AA.
AC Q05941;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR ACRA7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1 [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93147931; PubMed=7678857;
RA Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
RT "Molecular cloning, functional properties, and distribution of rat
RT brain alpha 7: a nicotinic cation channel highly permeable to
RT calcium.";
RL J. Neurosci. 13:596-604(1993).
RN 2 [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Boulter J.;
RN Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RP REVISION TO 363.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Hartley M.;
RN Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-
CC bungarotoxin. The structure is probably pentameric (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: S53987; AAB25224.2; -
CC EMBL: L31619; AAC33136.1; -
CC PIR: T01378; T01378.
CC InterPro: IPR006029; Neu_channel memb.
CC InterPro: IPR006202; Neur_chan_LBD.
CC InterPro: IPR006201; Neur_chan_LBD.
CC Pfam: PF02931; Neur_chan_LBD; 1.
CC Pfam: PF02932; Neur_chan memb; 1.
CC PRINTS: PR00252; NRIONCHANNEL.
CC TIGRFS: TIGR00860; LIC; 1.
CC PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
```


KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 502
FT
FT DOMAIN 23 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT TRANSMEM 318 469
FT TRANSMEM 470 490
FT DISULFID 150 164
FT DISULFID 212 213
FT CARBOHYD 46 46
FT CARBOHYD 90 90
FT CARBOHYD 133 133
FT CONFLICT 447 447
FT CONFLICT 469 469
SQ SEQUENCE 502 AA; 56410 MW; 00996E74EC7B9A56 CRC64;
Query Match 93.8%; Score 2535; DB 1; Length 502;
Best Local Similarity 93.6%; Pred. No. 4e-199;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;
QY 6 GGVWLAALSLHVSLOGEFQRLKYLKYNPLERPVANDSQPLTVVFSLSLLQIMDV 65
Db 6 GGVWLAALSLHVSLOGEFQRLKYLKYNPLERPVANDSQPLTVVFSLSLLQIMDV 65
QY 66 DEKQVLTNIWLSQSWTDHYLQNNVSEYGVKTVRFDGQIWKPDILLNSADRFAT 125
Db 66 DEKQVLTNIWLSQSWTDHYLQNNVSEYGVKTVRFDGQIWKPDILLNSADRFAT 125
QY 126 FHTNVLNNSGHCQVLPPIKPSVIVRWPFDPVQCKLFGSWSGWSLDLQMOEA 185
Db 126 FHTNVLNNSGHCQVLPPIKPSVIVRWPFDPVQCKLFGSWSGWSLDLQMOEA 185
QY 186 DISGYIPNGEWDVIGPKRSERFYECCKEPPDVTFTVMRRRTLYYGLNLLPCVLIS 245
Db 186 DISGYIPNGEWDVIGPKRSERFYECCKEPPDVTFTVMRRRTLYYGLNLLPCVLIS 245
QY 246 ALALIVFLPADSGKISLIGITVLSLTVFMLVAEIMPATSDSVPLIAQYFASMTIIVG 305
Db 246 ALALIVFLPADSGKISLIGITVLSLTVFMLVAEIMPATSDSVPLIAQYFASMTIIVG 305
QY 306 LSVVTVIVLVYHHDDPDGCKMPKTRVILLNWCWFLMKPBGDKVRPAQCHKQRCS 365
Db 306 LSVVTVIVLVYHHDDPDGCKMPKTRVILLNWCWFLMKPBGDKVRPAQCHKQRCS 365
QY 366 LASVEMSAVAPPASNGNLLYTGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHLLHGQ 425
Db 366 LASVEMSAVAPPASNGNLLYTGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHLLHGQ 425
QY 426 PPEGDPDLAKILEEVRVYIANTRCODESAVCEMKFACVVDRLCLMAFSVFTIICITG 485
Db 426 PPEGDPDLAKILEEVRVYIANTRCODESAVCEMKFACVVDRLCLMAFSVFTIICITG 485
QY 486 ILSAPNFVEAVSKDFA 502
Db 486 ILSAPNFVEAVSKDFA 502

RESULT 5

ID ACH7_CHICK
AC P22770;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
OX NCBI_TaxID=90311;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91097796; PubMed=1702646;
RA Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S., Millar N., Valera S., Barkas T., Ballivet M.;
RT "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmentally regulated and forms a homo-oligomeric channel blocked by alpha-BTX.";
RL Neuron 5:847-856(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90315158; PubMed=2369519;
RA Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
RT "Brain alpha-bungarotoxin binding protein cDNAs and MBs reveal subtypes of this branch of the ligand-gated ion channel gene superfamily.";
RL Neuron 5:35-48(1990).
RN [3]
RP SEQUENCE OF 1-18 FROM N.A.
RC STRAIN=White leghorn; TISSUE=Erythrocyte;
RX MEDLINE=93049204; PubMed=1425587;
RA Matter-Sadzikowski L., Hernandez M.C., Roztocil T., Ballivet M., Matter J.M.;
RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor promoter develops during morphogenesis of the central nervous system.";
RL EMBO J. 11:4529-4538(1992).
RN [4]
RP SEQUENCE OF 24-47.
RC TISSUE=Brain;
RX MEDLINE=85270494; PubMed=3860855;
RA Conti-Troconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A., Ray N., Raftery M.A.;
RT "Brain and muscle nicotinic acetylcholine receptors are different but homologous proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
RN [5]
RP MUTAGENESIS OF LSU-270.
RX MEDLINE=92049732; PubMed=1719423;
RA Recah P., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C., Hussey N., Bertrand S., Ballivet M., Changeux J.-P.;
RT "Mutations in the channel domain alter desensitization of a neuronal nicotinic receptor.";
RL Nature 353:846-849(1991).
RN [6]
RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
RX MEDLINE=93024917; PubMed=1383829;
RA Galzi J.-L., Devillers-Thiery A., Hussey N., Bertrand S., Changeux J.-P., Bertrand D.;
RT "Mutations in the channel domain of a neuronal nicotinic receptor convert ion selectivity from cationic to anionic.";
RL Nature 359:500-505(1992).
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma membrane.
CC -!- SUBUNIT: Forms a homo-oligomeric channel blocked by alpha-bungarotoxin. The structure is probably pentameric (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: Alpha-7 transcripts transiently accumulate in the developing optic tectum between E5 and E16.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
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EMBL; X52295; CAA36543.1; -
EMBL; X68246; CAA48317.1; -
EMBL; X68586; CAA48576.1; -
PIR; JN0113; JN0113.
PDB; 1KC4; 17-APR-02.
PDB; 1KL8; 17-APR-02.
InterPro; IPR006029; Neu_chan_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_LBD; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRfams; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; signal;
KW Transmembrane; Multigene family; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 502
FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT ALPHA-7 CHAIN.
FT DOMAIN 24 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT DOMAIN 318 469
FT TRANSMEM 470 490
FT DISULFID 150 164
FT CARBOHYD 46 46
FT CARBOHYD 90 90
FT CARBOHYD 133 133
FT MUTAGEN 270 270
FT CONFLICT 26 27
FT SEQUENCE 502 AA; 56946 MW; 572325D4309AD2FD CRC64;
Query Match 90.08; Score 2433; DB 1; Length 502;
Best Local Similarity 90.98; Pred. No. 8.3e-191;
Matches 450; Conservative 18; Mismatches 27; Indels 0; Gaps 0;
QY 8 VTLAALASLHVSILQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSLQLQIMDVDE 67
DB 8 LWLLAAGLVRESILQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSLQLQIMDVDE 67
QY 68 KNQVLTNNIWMQSWTDHYLQWNVSEYPGVKTVPFDPGQIWKPDILLYNSADERFDATFH 127
DB 68 KNQVLTNNIWMQSWTDHYLQWNVSEYPGVKNVRFDPGLIWKPDILLYNSADERFDATFH 127
QY 128 TNVLVNSGHCQYLPFGIFKSSCYIDVVRFPEDYHCKLFGWSYGSWSLQMQEADI 187
DB 128 TNVLVNSGHCQYLPFGIFKSSCYIDVVRFPEDYHCKLFGWSYGSWSLQMQEADI 187
QY 188 SGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVTMRRRTLYYGLNLLIPCVLISAL 247
DB 188 SGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVTMRRRTLYYGLNLLIPCVLISAL 247
QY 248 ALLVFLPADSGEKISIGITVLLSLTFVPMLLVAIMPATSDVPLIAQYFASFTMIIVGLS 307
DB 248 ALLVFLPADSGEKISIGITVLLSLTFVPMLLVAIMPATSDVPLIAQYFASFTMIIVGLS 307
QY 308 VVTVIVLYQHHPDDGKMPKWRVILLNWCANFLMRKPGEDKVRPACQKRRCSLA 367
DB 308 VVTVIVLYQHHPDDGKMPKWRVILLNWCANFLMRKPGEDKVRPACQKRRCSLS 367
QY 368 SVMESAVAPPASGNLYIYIGRGLDGVHCVPTPDGSGVVCGRMACSPHDBHLHGQPP 427
DB 368 SMENNTVSGQCNGNMLYIYIGRGLDGVHCVPTPDGSGVVCGRMACSPHDBHLHGQPP 427
QY 428 EGDPLAKILEVRYIANFRDQDEEAIENKWEKFAASVVDRLCLMAFSVFTICTIGIL 487

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Db 428 EGDPLAKILEVRYIANFRDQDEEAIENKWEKFAASVVDRLCLMAFSVFTICTIGIL 487
QY 488 MSAPNFVEAVSKDFA 502
Db 488 MSAPNFVEAVSKDFA 502

RESULT 6
ACHL_CAREL
ID ACHL_CAREL STANDARD; PRT; 498 AA.
AC P48180;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholine receptor like protein, alpha-type chain precursor.
GN F25G6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=96196478; PubMed=8627624;
RA Ballivet M., Alliod C., Bertrand S., Bertrand D.;
RT "Nicotinic acetylcholine receptors in the nematode Caenorhabditis
  elegans.";
RL J. Mol. Biol. 258:261-269(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nelson J., Wohldmann P.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Possible acetylcholine receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC
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EMBL; X83887; CAA58764.1; -
EMBL; AF022973; AAC25796.1; -
PIR; S68588; S68588.
HSP; P58154; I19B.
WormPep; F25G6.3; CE09639.
InterPro; IPR006029; Neu_chan_memb.
InterPro; IPR006202; Neur_chan_LBD.
InterPro; IPR006201; Neur_chan_LBD.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRfams; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW Transmembrane; Signal.
FT SIGNAL 1 19
FT CHAIN 20 498
FT POTENTIAL.
FT ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
FT ALPHA-TYPE CHAIN.
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 20 230
FT TRANSMEM 231 252
FT TRANSMEM 261 279
FT TRANSMEM 295 314
FT DOMAIN 315 472
FT TRANSMEM 473 493
FT DISULFID 147 161
FT DISULFID 211 212
FT CARBOHYD 43 43


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Db 487 PLYD 491

RESULT 8

ACH2 HUMAN STANDARD; PRT; 529 AA.

AC Q15822; O9HAQ3;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.

GN CHRNA2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Hypothalamus;

RX MEDLINE=97062879; PubMed=8906617;

RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,

RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;

RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta

RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional

RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and

RT beta 4 subunits.";

RL J. Mol. Neurosci. 7:217-228(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Groot Kormelink P.J.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Blechschmidt K., Rosenthal A.;

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an

CC extensive change in conformation that affects all subunits and

CC leads to opening of an ion-conducting channel across the plasma

CC membrane.

CC -!- SUBUNIT: Neuronal AChR seems to be composed of two different types

CC of subunits: alpha and non-alpha (beta). Alpha-2 subunit can be

CC combined to beta-2 or beta-4 to give rise to functional receptors.

CC -!- SURCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.

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CC -----

CC EMBL; U62431; ABA40109.1; -;

DR EMBL; Y16281; CAA76154.1; -;

DR EMBL; AF311103; -; NOT ANNOTATED_CDS.

DR Genew; HGNC:1956; CHRNA2.

DR MIM; 118502; -;

DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. . .; TAS.

DR GO; GO:0015464; F:acetylcholine receptor activity; TAS.

DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; TAS.

DR GO; GO:0007165; F:signal transduction; TAS.

DR GO; GO:0007268; F:synaptic transmission; TAS.

DR InterPro; IPR006029; Neur_chan_IIBD.

DR InterPro; IPR006201; Neur_chan_IIBD.

DR Pfam; PF02931; Neur_chan_IIBD; 1.

DR Pfam; PF02932; Neur_chan_IIBD; 1.

DR PRINTS; PR00252; NRIONCHANNEL.

DR TIGRFAMs; TIGR00860; LIC; 1.

DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.

KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;

Transmembrane; Multigene family.

KW SIGNAL 1 26 POTENTIAL.

FT CHAIN 27 529 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,

FT ALPHA-2 CHAIN.

FT DOMAIN 27 264 EXTRACELLULAR.

FT TRANSMEM 265 289 POTENTIAL.

FT TRANSMEM 297 315 POTENTIAL.

FT TRANSMEM 331 352 POTENTIAL.

FT DOMAIN 353 502 CYTOPLASMIC.

FT TRANSMEM 503 521 POTENTIAL.

FT DISULFID 183 197 BY SIMILARITY.

FT DISULFID 247 248 ASSOCIATED WITH RECEPTOR ACTIVATION

FT (BY SIMILARITY).

FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 125 125 A > T (IN REF. 3).

SQ SEQUENCE 529 AA; 59735 MW; 7F512B06CCD9A9AFD CRC64;

Query Match 35.1%; Score 949; DB 1; Length 529;

Best Local Similarity 40.0%; Pred. No. 9.3e-70;

Matches 201; Conservative 78; Mismatches 159; Indels 64; Gaps 9;

Qy 24 EFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDEKQVLTNTLWLSWT 83

Db 57 ETEDELFLKHLFRGYNRWAREPVNTSDVIVRFGLSIAQLIDVDKQNMNTVNLKQWS 116

Qy 84 DHVLQNVSEYPGVKTVRFPDGOIKWPKDILLYNASDERPDATFTNTLVNNSGHCYLP 143

Db 117 DYKLRNPADFGNITSRLVSEMIWIPDIVLYNADGEFAVTMTKAHLSTGTVHWVP 176

Qy 144 GIFKSCYIDVRWFPDVOHCKLFGSGWSYGGSLDLQMOE--ADISGYIPNGEWDLVGI 201

Db 177 AIYKSSCSIDVTFPPDQCKMKFGSWTYDKAKIDLEQMEQTVDLKDYWESGEWLVNA 236

Qy 202 PKRSERFYCCKEPYDVTFTVMRRRTLYGNNLLIPCVLSALALLVFLPADSGEK 261

Db 237 TGTYSKKYDCCABIYDVTYAFVIRLPLFTINLIIPCLLSCLTVLVFLPSDCGEK 296

Qy 262 ISLGITVLLSLTVFLLVVAIMPATSDSVPLIAQYFASFTMIIVGLSVVTVIVLQYHH 321

Db 297 ITICISVLLSLTVFLLITELIISTSLVPLIGEYLLFTMTFTLSIVIVFVLNVHRS 356

Qy 322 PDGKMPKTRVILLNWCAMFLMRKPGEDKVRPAQCHKQKRCRSLASVMSAVPPASN 381

Db 357 PSTHTMHWVKGALLGCVPRWLLNRP-----PPVEL 389

Qy 382 GNLLYI-----GPRGLDG-----VHCVPDPDSGVVGRMA-----CSPTHDEHLHGG 424

Db 390 CHPLRLKLSYHWLESNVDAEREVVVEEDRWACGHVAPSVGTLCSHG----LHSG 445

Qy 425 QP-----PEGD-----PDLAKILEEVRVIANFRQDESEAVCVSEWKAACVYDLCL 472

Db 446 ASGPKAEALLQEGELLSPHMQALEGVHVIADHLRSEDADSSVKEDKQVAMVIDRIFL 505

Qy 473 MAPSVFTIITIGILMSAPNFV 494

Db 506 WLFTIVFCFLGTIGLFL--PPFL 525

RESULT 9

ACH1_SCHGR STANDARD; PRT; 557 AA.

ID ACH1_SCHGR

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Acetylcholine receptor protein, alpha-1 chain precursor.

OS Schistocerca gregaria (Desert locust).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.

OX NCBI_TaxID=7010;

RN SEQUENCE FROM N.A.
 RP MEDLINE=91092263; PubMed=1702381;
 RA Marehall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
 RA Darlison M.G., Sattelle D.B., Barnard E.A.;
 RT "Sequence and functional expression of a single alpha subunit of an
 RT insect nicotinic acetylcholine receptor";
 RL EMBO J. 9:4391-4398(1990).
 CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
 CC extensive change in conformation that affects all subunits and
 CC leads to opening of an ion-conducting channel across the plasma
 CC membrane.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
 CC
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 CC
 CC -----
 DR EMBL; X55439; CAA39081.1; -.
 DR PIR; S12359; S12359.
 DR InterPro; IPR006029; Neu channel memb.
 DR InterPro; IPR006202; Neur chan LBD.
 DR InterPro; IPR006201; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUOTR ION CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 23
 FT CHAIN 24 557
 FT DOMAIN 24 244
 FT TRANSMEM 245 266
 FT TRANSMEM 274 294
 FT TRANSMEM 308 329
 FT TRANSMEM 330 500
 FT TRANSMEM 501 523
 FT DISULFID 151 165
 FT DISULFID 224 225
 FT CARBOHYD 47 47
 FT CARBOHYD 235 235
 FT DOMAIN 382 400
 FT DOMAIN 406 422
 FT SEQUENCE 557 AA; 63026 MW; 168389C887DFDF3E CRC64;
 SQ
 Query Match 35.1%; Score 949; DB 1; Length 557;
 Best Local Similarity 37.1%; Pred. No. 9.9e-70;
 Matches 201; Conservative 93; Mismatches 176; Indels 72; Gaps 6;
 QY 5 PGVWLAALASLLHSLQGEFORKLYKELVKNYPLERPVANDSQPLTVFSLSLQIMD 64
 Db PPMILLLLLLLHHHPAANPDARLVDLLSNVNLIRPVSNNITVAVKLGRLSLQID 65
 QY 65 VDEKNQVLTNWLQMSWDHYLQWVSEYPGVKTVPFDPGQIKWPDILYNSADRFDA 124
 Db LNKDQILATNWLHEWQDHKFRWPAEYGGVTELYPSEHITWLPDIYLNADGEYV 125
 QY 125 THTNVLVNSGHCQVLPICIFKSSCYIDVRPEPDVQHCCLKFGSMYGGWSLDLQ--- 181
 Db TWTAKVLAHTGKVVWTPPAIFKSSCEIDVRYFPFQDQCFMKFGSWTVDGQIDUKHN 185
 QY 182 -----MQEADISGVINGENDLVGIPGKRSEYECPEKYPDPVTFVTVMRRRTLYY 233
 Db QKDYDDNKVKGIDREYYSVSEVNDIILGVPAERHEKYPCCAEYPDIFENITLRRKTLF 245

QY 234 GLNLIPCVLISALALLVFLPADSGEKISIGITVLLSLTVFMLLVARIMPATSDSVPLI 293
 Db TVNLIVPCVGISYLSVLVFLPADSGEKIALCISLLSQTMFFLLISIIIPSTSLALPL 305
 QY 294 AQYFASWTMLIVGLSVTVTVLQYHHDDPGGKMPKTRVILLNWCANFLMRKPGE-- 350
 Db GYLLFTMLVGLSVTVITIMVNLVHYRKPSTHKMAPWVKVFIRRLPKLLMRVPEQLLA 365
 QY 351 DKVRPACQHKQKORCSLASVEMSAVAPPSPANGNLLYIGFRGLDGVCHVCTPTDPSGVVCGRM 410
 Db DLASKLLRLRHAHNSKLASAAAATAAASSS-----AASSPDS--LRHHH 408
 QY 411 ACSPTHDEHL-LHGGQPEG----- 429
 Db LHOHQHQLHQLHQLORPGCGNGLHSATNRFSGAGFGLPSVGLDGLSDVATRKXY 468
 QY 430 DPDLAKILLEEVRYIANRFCDSEAVCEKFAACVVDRLCLMAFSVFTIICITGILMS 489
 Db PFELEKALHNVLFIQNHMQRQDEDAEDQDGFVNWLDRLFLMFTTASIVGTFAIUCE 528
 QY 490 AP 491
 Db 529 AP 530
 RESULT 10
 ACH2 RAT
 ID ACH2 RAT STANDARD; PRT; 511 AA.
 AC P12389; O08952;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
 GN CHRNA2 OR ACRA2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=88178113; PubMed=2832952;
 RA Wada K., Halliwell M., Boulter J., Connolly J.G., Wada E.,
 RA Deneris E.S., Swanson L.W., Heinemann S.F., Patrick J.;
 RT "Functional expression of a new pharmacological subtype of brain
 RT nicotinic acetylcholine receptor.";
 RL Science 240:330-334(1988).
 RN [2]
 RP REVISIONS.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RA Boulter J.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
 CC extensive change in conformation that affects all subunits and
 CC leads to opening of an ion-conducting channel across the plasma
 CC membrane.
 CC -!- SUBUNIT: Neuronal AChR seems to be composed of two different types
 CC of subunits: alpha and non-alpha (beta). Alpha-2 subunit can be
 CC combined to beta-2 or beta-4 to give rise to functional receptors.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
 CC
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 CC
 CC -----
 DR EMBL; L10077; AAB60900.1; -.
 DR EMBL; M20297; AAA40664.1; -.
 DR EMBL; M20292; AAA40664.1; JOINED.

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DR EMBL; M20293; AAA40664.1; JOINED.
DR EMBL; M20294; AAA40664.1; JOINED.
DR EMBL; M20295; AAA40664.1; JOINED.
DR EMBL; M20296; AAA40664.1; JOINED.
DR PIR; A40110; A40110.
DR InterPro; IPR006029; Neu_chan_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_chan_LBD.
DR Pfam; PF02931; Neu_chan_LBD; 1.
DR Pfam; PF02932; Neu_chan_memb; 1.
DR PRINTS; PR00252; NR1ONCHANNEL.
DR TIGRfams; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 27
FT CHAIN 28 511
FT DOMAIN 28 241
FT TRANSMEM 242 266
FT TRANSMEM 274 292
FT TRANSMEM 308 329
FT DOMAIN 330 484
FT TRANSMEM 485 503
FT TRANSMEM 391 402
FT DISULFID 160 174
FT DISULFID 224 225
FT CARBOHYD 56 56
FT CARBOHYD 106 106
FT CARBOHYD 212 212
FT CONFLICT 494 494
SQ SEQUENCE 511 AA; 58611 MW; 382483B901D613B CRC64;

Query Match 35.0%; Score 944.5; DB 1; Length 511;
Best Local Similarity 39.1%; Pred. No. 2.1e-69;
Matches 202; Conservative 82; Mismatches 179; Indels 53; Gaps 9;

Qy 8 VW--LALAASLLHVSQGEFORKLYKELVKNYNFLERPVANDSOPLTVYFSLSLQIMDV 65
Db 16 LWCLLLVPAVLTVQQGSHTHAEDRLFGLFGGYNWARVPVNTSDVIVRFLSLAQILDV 75

Qy 66 DEKNQVLTNNLQMSWDHYLQWVSEYFGKTVRPPDQIWKPDILLNSABERDAT 125
Db 76 DEKNQMTNNLQWMDYKLRDPAPFEGNVTSLRVPSEMIWPDIVLYNNADGEFAVT 135

Qy 126 FHTNVLVNSGHCVOYLPFGIEKSCYIDVRFPDQVQCKLFGSGWSYGLDQMOE- 184
Db 136 HMTKAHLFFGTGVHVPVPAIYKSSCSIDVTFPPDQCNCKKFGSWTYDKAKIDLEQWER 195

Qy 185 -ADISGYIPNGEWDLVGIPGKRSEFYECCKEYPPDVFTVTMRRTLYYGLNLLIPCVL 243
Db 196 TVDLKDYWESGEWALINATGYNKKYDCCAEIYPDVTYFVIRRLPLFYINLIIPCLL 255

Qy 244 ISALALVFLPADSGEKISLIGITVLLSLVFMILLVAIMPATSDSVPLIAQYFASMTII 303
Db 256 ISCLTVLVFLYLPSECGEKITLCISVLLSLVFLLLITIIPTSLVPLIGEYLLFTMIF 315

Qy 304 VGLSVVTVIVLVQHHDPDGGKPKWTRVILLNWCAMFLRMKRP-----GEDKVRPA 356
Db 316 VTLISVITVFLNVHRSFSTHNMENWVRVALLGVRPRLMMNRPLPFWMLHGSFDLXLS 375

Qy 357 COHKORRCSLASVEMSAVAPPASNGNLLYTGFRGLDGVCVFTPDG--GVVCGRMACSP 414
Db 376 PSYHWMLETNMDAGEREEETEEEDENICV-----CAGLPDSSMGVLYG----- 420

Qy 415 THDEHLLGG-----QPEEG-----DPDLAKILEVRYIANFRQDSEAVCS 458
Db 421 -----HGLHLRAMEPETKTPSOASBILISPOIQKALEGVHYIADLRSEDADSSVKE 473

Qy 459 EWKFAACVVDRLCLMAFVFTTICTIGTIGLMSAPNEV 494
Db 474 DKYVAMVVDRLCLMAFVFTTICTIGTIGLMSAPNEV 494
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RESULT 11
ACHN CARAU STANDARD; PRT; 459 AA.
ID ACN CARAU STANDARD; PRT; 459 AA.
AC P19370;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, beta-2 chain (GF-beta-2)
DE (Fragment).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=90384858; PubMed=2402468;
RA Hieber V.C., Bouchev J.E., Agranoff B.W., Goldman D.;
RT "Nucleotide and deduced amino acid sequence of the goldfish neural
RL nicotinic acetylcholine receptor beta-2 subunit.";
RL Nucleic Acids Res. 18:5307-5307(1990)
CC -|- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -|- SUBUNIT: Neuronal AChR seems to be composed of two different type
CC of subunits: alpha and non-alpha (beta).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC -----
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CC -----
EMBL; X54052; CAA37986.1; -.
PIR; S14703; S14703.
DR InterPro; IPR006029; Neu_chan_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_chan_LBD.
DR Pfam; PF02931; Neu_chan_LBD; 1.
DR Pfam; PF02932; Neu_chan_memb; 1.
DR PRINTS; PR00252; NR1ONCHANNEL.
DR TIGRfams; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
KW Transmembrane; Multigene family.
FT NON_TER 1 203
FT DOMAIN <1 203 EXTRACELLULAR.
FT TRANSMEM 204 228
FT TRANSMEM 236 254
FT TRANSMEM 270 291
FT DOMAIN 292 421
FT TRANSMEM 422 440
FT TRANSMEM 441 459
FT CARBOHYD 21 21
FT CARBOHYD 125 139
FT DISULFID 138 138
FT CARBOHYD 138 138
SQ SEQUENCE 459 AA; 53040 MW; 860B1A011AA47CF6 CRC64;

Query Match 34.9%; Score 942.5; DB 1; Length 459;
Best Local Similarity 38.7%; Pred. No. 2.6e-69;
Matches 190; Conservative 95; Mismatches 141; Indels 65; Gaps 8;

Qy 35 KYNPLRPVANDSQPLTVYFSLSLQIMDVDEKNQVLTNNLQMSWDHYLQWVSEY 94
Db 10 ERYNKLIRPAVNVKQQVTIGIKVSLAQISNREQIMTNNVLTQETDYLRLVDPNEY 69
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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=90301489; PubMed=21114015;
RT Baumann A., Jonas P., Gundelfinger E.D.;
RT "Sequence of D alpha 2, a novel alpha-like subunit of Drosophila
RL nicotinic acetylcholine receptors.";
RL Nucleic Acids Res. 18:3640-3640(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=90353591; PubMed=2117557;
RT Jonas P., Baumann A., Merz B., Gundelfinger E.D.;
RT "Structure and developmental expression of the D alpha 2 gene
RT encoding a novel nicotinic acetylcholine receptor protein of
RT Drosophila melanogaster.";
RL FEBS Lett. 269:264-268(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90360975; PubMed=1697262;
RA Sawruk E., Schloss P., Betz H., Schmitt B.;
RT "Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD,
RT a novel developmentally regulated alpha-subunit.";
RL EMBO J. 9:2671-2677(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballen R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berland B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang X., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphry L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.-H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley; TISSUE=Head;
RX MEDLINE=90353591; PubMed=2117557;
RT Jonas P., Baumann A., Merz B., Gundelfinger E.D.;
RT "Structure and developmental expression of the D alpha 2 gene
RT encoding a novel nicotinic acetylcholine receptor protein of
RT Drosophila melanogaster.";
RL FEBS Lett. 269:264-268(1990).

Db 201 HISQKNDKDKVEIGDLREYPSVEMDILGPAERHEKYPPCCAPYDPDIFFETILRRK 260
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 Db 261 TLFVTNLIIPCVGISVLSVFLPADSGEKIALCISILSQTMTFFLLISEITPSTSLA 320
 QY 290 VPLIAQFASTMIIVGLSVVTVIVLQVHHDPDGGKMPKTRVILLNWCACAFURMKRPG 349
 Db 321 LPLLGKYLFTMLVGLSVITIIILMIHYRKPSTHWRPWRPIRFFFKRLPKLLMRVP- 379
 QY 350 EDKVRPACQHKQR-----RCSLASVEMSAVAPPPASNGNLL-YIGFRLDGVHC 397
 Db 380 KDLRLDLAANKINYGLKFSKTKFGQALMDENQMNSSGSSPSDLRMRQGRVGGCGNGHV 439
 QY 398 VPTPD--SGVV-----CGRMACSPTHDEHLHGGQPEGDPDLAKLLEVRV 442
 Db 440 TTATNRFSGLVAGLGGGLSTUSGNGLPVSUGLSDLSVDAARKKYPPFELEKAHNVMF 499
 QY 443 IANFRQDESEAVCSEWKFAACVVDRCLMAFSVFTIICVTIGILMGAPEVE 495
 Db 500 IQHEMRQDEFAEDQDQMGFVAMVMDRLFLWLFMIASIVGTFVILGEAPSLYD 552

RESULT 15

ACH3 HUMAN
 ID ACH3 HUMAN STANDARD; PRT; 503 AA.
 AC P32297; Q15823; Q96RH3; Q95553; Q9BQ93;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
 GN CHRNA3 OR NACHRA3
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=90245296; PubMed=2336208;
 RA Fornasari D., Chini B., Tarroni P., Clementi F.;
 RT "Molecular cloning of human neuronal nicotinic receptor alpha
 3-subunit.";
 RL Neurosci. Lett. 111:351-356(1990).
 [2]
 SEQUENCE FROM N.A. (ISOFORM 1).
 TISSUE=Thymus;
 MEDLINE=91114756; PubMed=1989896;
 RA Mihovilovic M., Roses A.D.;
 RT "Expression of mRNAs in human thymus coding for the alpha 3 subunit
 of a neuronal acetylcholine receptor.";
 RL Exp. Neurol. 111:175-180(1991).
 [3]
 SEQUENCE FROM N.A. (ISOFORM 2).
 MEDLINE=97062879; PubMed=8906617;
 RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
 RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 beta 4 subunits";
 RL J. Mol. Neurosci. 7:217-228(1996).
 [4]
 SEQUENCE FROM N.A. (ISOFORM 1).
 MEDLINE=97162233; PubMed=9009220;
 RA Groot Kormelink P.J., Luyten W.H.M.L.;
 RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
 nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
 expression of seven nAChR subunits in the human neuroblastoma cell
 line SH-SY5Y and/or IMR-32.";
 RL FEBS Lett. 400:309-314(1997).
 [5]
 SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=99118870; PubMed=9921897;
 RA Rempel N., Heyers S., Engels H., Sleegers E., Steinlein O.K.;
 RT "The structures of the human neuronal nicotinic acetylcholine receptor
 beta2- and alpha3-subunit genes (CHRNA2 and CHRNA3).";
 RL Hum. Genet. 103:645-653(1998).
 [6]
 SEQUENCE FROM N.A., AND VARIANT LEU-21 INS.
 MEDLINE=21342809; PubMed=11450844;
 RA Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
 RT "Characterization of the human beta4 nAChR gene and polymorphisms in
 CHRNA3 and CHRNA4.";
 RL J. Hum. Genet. 46:362-366(2001).
 [7]
 SEQUENCE FROM N.A. (ISOFORM 2).
 TISSUE=Lung;
 MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [8]
 SEQUENCE OF 30-503 FROM N.A.
 TISSUE=Brain;
 RA Anand R., Lindstrom J.;
 RT Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
 [9]
 SEQUENCE OF 6-493 FROM N.A.
 TISSUE=Epidermal keratinocytes;
 RA Arredondo J., Grando S.A.;
 RT "Cloning cholinergic receptors in human keratinocytes.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
 CC extensive change in conformation that affects all subunits and
 CC leads to opening of an ion-conducting channel across the plasma
 CC membrane.
 CC -!- SUBUNIT: Neuronal AChR seems to be composed of two different type
 CC of subunits: alpha and non-alpha (betaA).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=P32297-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P32297-2; Sequence=VSP_000073;
 CC Note=No experimental confirmation available;
 CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M86383; AAC84176.1; --
 CC EMBL; M37981; AAA59942.1; --
 DR

[illegible]

DR	EMBL; U62432; AAB40110.1; -.
DR	EMBL; Y08416; CAA9695.1; -.
DR	EMBL; AJ007783; CAA07682.1; -.
DR	EMBL; AJ007784; CAA07682.1; JOINED.
DR	EMBL; AJ007785; CAA07682.1; JOINED.
DR	EMBL; AJ007786; CAA07682.1; JOINED.
DR	EMBL; AJ007787; CAA07682.1; JOINED.
DR	EMBL; BC001642; AAH01642.1; -.
DR	EMBL; BC002996; AAH02996.1; -.
DR	EMBL; BC000513; AAH00513.1; -.
DR	EMBL; AF385584; AAK68110.1; -.
DR	EMBL; X53559; CAA37625.1; -.
DR	PIR; A37040; A37040.
DR	PIR; A53956; A53956.
DR	Genew; HGNC:1957; CHRNA3.
DR	MIM; 118503.
DR	GO; GO:0005992; Cnictinic acetylcholine-gated receptor-chan. . ; TAS.
DR	GO; GO:0015464; Fnicetylcholine receptor activity; TAS.
DR	GO; GO:0004889; Fnicictinic acetylcholine-activated cation-se. . ; TAS.
DR	GO; GO:0005215; F-transporter activity; TAS.
DR	GO; GO:0007165; P-signal transduction; TAS.
DR	GO; GO:0006810; P-transport; TAS.
DR	InterPro; IPR006029; Neu_chan_memb.
DR	InterPro; IPR006202; Neur_chan_LBD.
DR	InterPro; IPR006201; Neur_channel.
DR	Pfam; PF02931; Neur_chan_LBD; 1.
DR	Pfam; PF02932; Neur_chan_memb; 1.
DR	PRINTS; PR00252; NRIONCHANNEL.
DR	TIGRFAMS; TIGR00860; LIC; 1.
DR	PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR	KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
DR	KW Transmembrane; Multigene family; Alternative splicing; Polymorphism.
FT	SIGNAL 1 29 POTENTIAL.
FT	CHAIN 30 503 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT	DOMAIN 30 238 ALPHA-3 CHAIN
FT	TRANSMEM 239 263 EXTRACELLULAR (POTENTIAL).
FT	TRANSEM 271 289 POTENTIAL.
FT	TRANSEM 305 326 POTENTIAL.
FT	DOMAIN 327 475 CYTOPLASMIC (POTENTIAL).
FT	TRANSEM 476 495 POTENTIAL.
FT	DISULFID 157 171 BY SIMILARITY.
FT	DISULFID 221 222 ASSOCIATED WITH RECEPTOR ACTIVATION
FT	CARBOHYD 53 53 (BY SIMILARITY).
FT	CARBOHYD 170 170 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPLIC 1 5 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	MAIAP -> MGSGPL (in isoform 2).
FT	/FtId=VSP_000073.
FT	L -> LL.
FT	/FtId=VAR_013240.
FT	VSLPALUSP -> ALAAPGAVA (IN REF. 2).
FT	LSPP -> CRA (IN REF. 1).
FT	D -> G (IN REF. 1).
FT	DD -> TT (IN REF. 1).
FT	I -> S (IN REF. 1).
FT	L -> V (IN REF. 1).
FT	SEQUENCE 503 AA; 57309 MW; 8A9BEC5D71AE7D6 CRC64;
Query Match	34.6%; Score 936; DB 1; Length 503;
Best Local Similarity	37.7%; Pred. No. 1e-68;
Matches 189; Conservative	94; Mismatches 164; Indels 54; Gaps 7;
QY 10	LALAASILLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTYVFSLLIQMDVDEN 69
Db 17	LLLLLSLLPVARASEAHRLUFEDYEIRPEVANVSDVIIHFVEVMSQLVKVDEVN 76
QY 70	QVLTTTIIWLQMSWDTHYLDQNVSSYPGVKTFRFPDGQIKWKPDILLXNSADRRFDATHTN 129
Db 77	QIMETNLMLAQIWNDYKLWNPSDYGAEPFEVPAQIKWKPDIVLXNAVCGDFQVDKTK 136
QY 130	VLNNSHGCQYLPPIPKSCCYIDVRWPFDPDVQHCKLKFGSWSYGGWSLDIQM--QRADI 187
Db 137	ALKAYTGVTWIPPAIFKSKCIDVTFPYDQNTKFKGSWYDKAKIDLVLIGSSMNL 196

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:27:17 ; Search time 45 Seconds
(without alignments)
3519.781 Million cell updates/sec

Title: US-09-703-951A-12

Perfect score: 2702

Sequence: 1 MRCSPGGVWLALASLHVS.....TIGILMSAPNFVEAVSKDPA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mmc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertibrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2679	99.1	502	6 Q866A2	Q866A2 macaca mula
2	2550	94.4	502	11 Q9JHD6	Q9JHD6 mus musculus
3	2077.5	76.9	509	13 Q800C7	Q800C7 brachydanio
4	1849	68.4	513	13 Q7T289	Q7T289 fugu rubrip
5	1820.5	67.4	511	13 Q03481	Q03481 gallus gall
6	1769.5	65.5	486	13 Q7T280	Q7T280 fugu rubrip
7	1734	64.2	555	13 Q7T2U0	Q7T2U0 fugu rubrip
8	1705	63.1	321	4 Q8IU24	Q8IU24 homo sapien
9	1575.5	58.3	554	13 Q7T2T9	Q7T2T9 fugu rubrip
10	1569.5	58.1	474	13 Q7T2U1	Q7T2U1 fugu rubrip
11	1271	47.0	542	5 Q86MN7	Q86MN7 drosophila
12	1270.5	47.0	545	5 Q9VW19	Q9VW19 drosophila
13	1264	46.8	807	5 Q87V5	Q87V5 drosophila
14	1258.5	46.6	501	5 Q9XZ14	Q9XZ14 heliothis v
15	1246	46.1	496	5 Q9XZ13	Q9XZ13 heliothis v
16	1225	45.3	494	5 Q87S2	Q87S2 drosophila

17	1223	45.3	494	5	Q8T7S3	Q8T7S3 drosophila
18	1221	45.2	494	5	Q86MN8	Q86MN8 drosophila
19	1218	45.1	494	5	Q8T7S1	Q8T7S1 drosophila
20	1208.5	44.7	509	5	Q8T7S0	Q8T7S0 drosophila
21	1206.5	44.7	523	5	Q8T7R9	Q8T7R9 drosophila
22	1097	40.6	554	5	Q82083	Q82083 caenorhabdi
23	1021.5	37.8	480	5	Q81932	Q81932 caenorhabdi
24	999	37.0	461	5	Q81197	Q81197 caenorhabdi
25	976.5	36.1	523	5	Q46128	Q46128 heliothis v
26	958	35.5	554	5	Q3VL79	Q3VL79 drosophila
27	953.5	35.3	568	5	Q9NFR5	Q9NFR5 drosophila
28	952.5	35.3	545	5	Q96631	Q96631 heliothis v
29	951.5	35.2	536	5	Q8T0Y9	Q8T0Y9 aplysia cal
30	951	35.2	515	5	Q46133	Q46133 locusta mig
31	945	35.0	537	5	Q8MUR0	Q8MUR0 apis mellif
32	945	35.0	542	5	Q18556	Q18556 caenorhabdi
33	943.5	34.9	552	5	Q91765	Q91765 myzus persi
34	942.5	34.9	537	5	Q90941	Q90941 myzus persi
35	942	34.9	505	4	Q86U77	Q86U77 homo sapien
36	941.5	34.8	536	5	Q8T9S0	Q8T9S0 aplysia cal
37	937	34.7	512	11	Q91X60	Q91X60 mus musculu
38	930.5	34.4	520	13	Q7Z2P7	Q7Z2P7 brachydanio
39	924	34.2	795	5	Q18394	Q18394 drosophila
40	922.5	34.1	504	11	Q8BV44	Q8BV44 mus musculu
41	921.5	34.1	499	11	Q8VHH6	Q8VHH6 mus musculu
42	921	34.1	495	11	Q8R493	Q8R493 mus musculu
43	921	34.1	502	5	Q9N587	Q9N587 caenorhabdi
44	920	34.0	439	13	Q7T2S5	Q7T2S5 fugu rubrip
45	919	34.0	540	5	Q46134	Q46134 locusta mig

ALIGNMENTS

RESULT 1

ID Q866A2 PRELIMINARY; PRT; 502 AA.
AC Q866A2; DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Nicotinic acetylcholine receptor alpha7.
GN CHRNA7.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Prokocil B.J., Sekhon H.S., Keller J.A., Jia Y., Blakely R.D.,
RA Lindstrom J., Spindel E.R.,
RT "An Intrinsic Non-neuronal Nicotinic Cholinergic Signaling System in
RT Monkey Lung Airway Epithelium";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF486623; AA084497.1; -
DR GO; GO:0016030; C:membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. .; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_channel_LBD.
DR InterPro; IPR006029; Neu_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRPFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR Receptor.
SQ SEQUENCE 502 AA; 56429 MW; 213C8A282242AC4A CRC64;
Query Match 99.1%; Score 2679; DB 6; Length 502;
Best Local Similarity 99.0%; Pred. No. 2.9e-229;

Matches 497; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSPGGWLAALASLLHVSLOGEFQRLKYLKVNINPLERPVANDSQPLTVYFSLSL 60
 |||||
 Db 1 MRCSPGGWLAALASLLHVSLOGEFQRLKYLKVNINPLERPVANDSQPLTVYFSLSL 60
 |||||

QY 61 QIMDVDEKQVLTNTNWLQMSWDHYLQWNVSEYGVKTVRFPDGOIKWPDILLYNSADE 120
 |||||
 Db 61 QIMDVDEKQVLTNTNWLQMSWDHYLQWNVSEYGVKTVRFPDGOIKWPDILLYNSADE 120
 |||||

QY 121 RFDATEHTNVLNNSGHCQVLPFGIFKSSCYIDVRWFFPDVQCKLKFGWSYGVGWSL 180
 |||||
 Db 121 RFDATEHTNVLNNSGHCQVLPFGIFKSSCYIDVRWFFPDVQCKLKFGWSYGVGWSL 180
 |||||

QY 181 QMGEADISGYPNGEWDLVGIPGRSERFVECKEPEYDVTFTVWRRRTLYYGLNLLIP 240
 |||||
 Db 181 QMGEADISGYPNGEWDLVGIPGRSERFVECKEPEYDVTFTVWRRRTLYYGLNLLIP 240
 |||||

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 300
 |||||
 Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 300
 |||||

QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLMRKRPGEKVRPACQHK 360
 |||||
 Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLMRKRPGEKVRPACQHK 360
 |||||

QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFGLDGVHCYPTPDGSGVCGRMACSPTHDEHL 420
 |||||
 Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFGLDGVHCYPTPDGSGVCGRMACSPTHDEHL 420
 |||||

QY 421 LHGGQPEGDPDLAKILEEYRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 |||||
 Db 421 LHGGQPEGDPDLAKILEEYRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 |||||

QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 |||||
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502
 |||||

RESULT 2

Q9JHD6 PRELIMINARY; PRT; 502 AA.

AC Q9JHD6; MEDLINE=97189245; PubMed=9037516;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Nicotinic acetylcholine receptor subunit alpha 7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D8A/21bg;
 RX MEDLINE=97189245; PubMed=9037516;
 RA Stitzel J.A., Farnham D.A., Collins A.C.;
 RT "Linkage of strain-specific nicotinic receptor alpha 7 subunit
 restriction fragment length polymorphisms with levels of alpha-
 bungarotoxin binding in brain."
 RL Brain Res. Mol. Brain Res. 43:30-40 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D8A/21bg;
 RA Stitzel J.A.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 DR EMBL; AF225980; AAF35885.1; --
 DR MGI; MGI:199779; Chnra7.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. .; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.

DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0007268; P:synaptic transmission; IEA.
 DR InterPro; IPR006201; Neur_chan_LBD.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_LBD; 1.
 DR PRINTS; PR0252; NRIONCHANNEL.
 DR TIGRFAM; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
 KW Transmembrane.
 SQ SEQUENCE 502 AA; 56617 MW; C9353B5136D620E3 CRC64;

Query Match 94.4%; Score 2550; DB 11; Length 502;
 Best Local Similarity 94.0%; Pred. No. 8.2e-218;
 Matches 467; Conservative 19; Mismatches 11; Indels 0; Gaps 0;

QY 6 GGVWLALASLLHVSLOGEFQRLKYLKVNINPLERPVANDSQPLTVYFSLSLQIMDV 65
 |||||
 Db 6 GGVWLALASLLHVSLOGEFQRLKYLKVNINPLERPVANDSQPLTVYFSLSLQIMDV 65
 |||||

QY 66 DEKNQVLTNTNWLQMSWDHYLQWNVSEYGVKTVRFPDGOIKWPDILLYNSADERFAT 125
 |||||
 Db 66 DEKNQVLTNTNWLQMSWDHYLQWNVSEYGVKTVRFPDGOIKWPDILLYNSADERFAT 125
 |||||

QY 126 FHTNVLNNSGHCQVLPFGIFKSSCYIDVRWFFPDVQCKLKFGWSYGVGWSLQMOEA 185
 |||||
 Db 126 FHTNVLNNSGHCQVLPFGIFKSSCYIDVRWFFPDVQCKLKFGWSYGVGWSLQMOEA 185
 |||||

QY 186 DISGYIPNGEWDLVGIPGRSERFVECKEPEYDVTFTVWRRRTLYYGLNLLIPCVLIS 245
 |||||
 Db 186 DISGYIPNGEWDLVGIPGRSERFVECKEPEYDVTFTVWRRRTLYYGLNLLIPCVLIS 245
 |||||

QY 246 ALALLVFLPADSGEKISLGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 305
 |||||
 Db 246 ALALLVFLPADSGEKISLGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 305
 |||||

QY 306 LSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLMRKRPGEKVRPACQHKRCS 365
 |||||
 Db 306 LSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLMRKRPGEKVRPACQHKRCS 365
 |||||

QY 366 LASVEMSAVAPPASNGNLLYIGFGLDGVHCYPTPDGSGVCGRMACSPTHDEHLHGQ 425
 |||||
 Db 366 LASVEMSAVAPPASNGNLLYIGFGLDGVHCYPTPDGSGVCGRMACSPTHDEHLHGQ 425
 |||||

QY 426 PPEGDPDLAKILEEYRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 485
 |||||
 Db 426 PPEGDPDLAKILEEYRYIANFRQCDESEAVCSWKFAACVVDRLCLMAFSVFTI 485
 |||||

QY 486 ILMSAPNFVEAVSKDFA 502
 |||||
 Db 486 ILMSAPNFVEAVSKDFA 502
 |||||

RESULT 3

Q800C7 PRELIMINARY; PRT; 509 AA.

AC Q800C7; MEDLINE=97189245; PubMed=9037516;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Nicotinic acetylcholine receptor alpha 7 subunit.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zirger J.M., Boyd R.T.;
 RT "Cloning and expression of zebrafish neuronal nicotinic acetylcholine

```

RT receptors."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY247962; AAC91913.1; -.
DR GO: 0016020; C.membrane; IEA.
DR GO: 0005230; F.extracellular ligand-gated ion channel acti. .; IEA.
DR GO: 0030594; F.neurotransmitter receptor activity; IEA.
DR GO: 0006811; P:ion transport; IEA.
DR InterPro: IPR006201; Neur channel.
DR InterPro: IPR006202; Neur channel.
DR InterPro: IPR006029; Neu_chan_LBD; 1.
DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan memb; 1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR TIGRFAMs: TIGR00860; LIC; 1.
DR PROSITE: PS00236; NEUOTR_ION_CHANNEL; 1.
KW Receptor.
SQ SEQUENCE 509 AA; 58056 MW; 1BF152F4245578BA CRC64;

Query Match 76.9%; Score 2077.5; DB 13; Length 509;
Best Local Similarity 76.2%; Pred. No. 7.9e-176;
Matches 387; Conservative 51; Mismatches 55; Indels 15; Gaps 5;

QY 7 GVW-----LALASLLHVSLOGEQRKLYKELVKNYNPLRPVANDSOPLTVYFSLSLQ 61
DB 2 GIWEYTLFTTCCLSVSLSGEQRRLYRDLMDKYNPLRPVFNDSLSLTVYFMSLMQ 61
QY 62 IMDVDEKNQVLTINILQMSWTDHYLOWNVSEYFGVKTVPDPDQIWKPDILLYNSADER 121
DB 62 IMDVDEKNQVLTINILQWYDYLYLOWNVSEYFGVKTVPDPDQIWKPDILLYNSADER 121
QY 122 FDATAFTNVLNNSGHCQYLPPIGKSCYIDVRFPPDVQVHCKLKFGWSYGGSLDLQ 181
DB 122 FDATAFTNVLNNSGACQYLPPIGKSCYIDVRFPPDQVHCKLKFGWSYGGSLDLQ 181
QY 182 MQEADISYINGEWDLVIGPKSEREYECCKEYPDVTVTWMRRRTLYYGLNLLIPC 241
DB 182 MIDADITGIYANGSWDLVEVGRNERYDCCKEYPDVTVTWMRRRTLYYGLNLLIPC 241
QY 242 VLISALALLVFLPADSGEKLISGLITVLLSLTFVMLVAEIMPATSDSVPLIAQVFASTM 301
DB 242 VLISALALLVFLPADSGEKLISGLITVLLSLTFVMLVAEIMPATSDSVPLIAQVFASTM 301
QY 302 IIVGLSVVTVVLYHHDDPGGKMPKWTVRVILLNWCWFLMRKPGEDKVRPAQCHQK 361
DB 302 VIVGLSVIATVWLYQYHYHDPGGKMPKWTVRVILLNWCWFLMRKPGEDKVRPAQCHQK 361
QY 362 PRCSLASVEMSAVAPPPA--SNGNLLYIGFGRGLDGVHCVPTPDSGVVCGRMACSFTHDEH 419
DB 362 PRSLSSVDLN--ISPGVAQSTNGNLLYIGFGRMDTIHYATSPDSGVICSLRVATGEEDV- 419
QY 420 LLHGGQPPE-----GDPDLAKILEEVRYIANRPRCQDESAVCSEWKFACVVDRLCLM 473
DB 420 LLPGAQASVSSSGPGEFELSCLLDEVIYISKRFDQDBEDTVCNEMKFAASVIDRLCLM 479
QY 474 AFSVFTIICITIGILMSAPNFVEAVSKDF 501
DB 480 AFSLFTIICITIGILMSAPNFVEAVSKDF 507

RESULT 4
Q/T2R9 PRELIMINARY; PRT; 513 AA.
AC Q/T2R9;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DE Nicotinic acetylcholine receptor alpha 8b subunit (Fragment).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
NCBI_TaxID=31033;

[1]
RN SEQUENCE FROM N.A.
RP Jones A.K., Elgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
RT Fugu rubripes.";
RL Genomics 0:0-0(2003).
DR EMBL: AY299466; AAP58381.1; -.
KW Receptor.
FT NON TER
SQ SEQUENCE 513 AA; 57294 MW; 03315A831E0CA499 CRC64;

Query Match 68.4%; Score 1849; DB 13; Length 513;
Best Local Similarity 68.7%; Pred. No. 1.6e-155;
Matches 356; Conservative 47; Mismatches 73; Indels 42; Gaps 7;

QY 20 SLOGEQRKLYKELVKNYNPLRPVANDSOPLTVYFSLSLQIMVDKQVLTINILQ 79
DB 1 SLOGEQRKLYKELVKNYNPLRPVANDSOPLTVYFSLSLQIMVDKQVLTINILQ 60
QY 80 MSMTDHYLOWNVSEYFGVKTVPDPDQIWKPDILLYNSADERFDATAFTNVLNNSGHCQ 139
DB 61 LYMTDIYLTWNPSYPGVQNLRPDPDQVTPDILLYNSADERFDATAFTNVLNNSGVCQ 120
QY 140 YLPPGIFKSCYIDVRFPPDVQVHCKLKFGWSYGGSLDLQMQEADISYINGEWDLV 199
DB 121 YIPPGILKSTCYIDVRFPPDVQVHCKLKFGWSYGGSLDLQMQEADISYINGEWDLV 180
QY 200 GIPKSEREYECCKEYPDVTVTWMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 259
DB 181 GVPKRNELDYDCCKEYPDVTVTWMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 240
QY 260 EKISGLITVLLSLTFVMLVAEIMPATSDSVPLIAQVFASTMITVGLSVVTVVLYQVHH 319
DB 241 EKISGLITVLLSLTFVMLVAEIMPATSDSVPLIAQVFASTMITVGLSVVTVVLYQVHH 300
QY 320 HDPPGKMPKWTVRVILLNWCWFLMRKPGEDKVRPA--COH-KORCSLASVEMSAV-- 374
DB 301 HDPPGKMPKWTVRVILLNWCWFLMRKPGEDKVRPA--COH-KORCSLASVEMSAV-- 360
QY 375 -----APPPASNGNL--LYIGFGRGLDGVHCVPTPDSGVVCGRMACSFTHDEH 419
DB 361 LSVPLIAQVTSQPSCTGTSNGSMGYFTYHTPTDSSSCPPSDSGVALGGRNHSFSEE-- 418
QY 420 LLHGGQPPE-----DPLAKILEEVRYIANRPRCQDESAVCSEWKFACVVDRLCLM 463
DB 419 ----AEPVGGSGSLGMVGVRVSIPPEIMCILEEVSYIAQRFDDQDEAICSEWKFACV 474
QY 464 ACVVDRLCLMFAVSFTIICITIGILMSAPNFVEAVSKDF 501
DB 475 AAVVDRLCLMFAVSFTIICITIGILMSAPNFVEAVSKDF 512

RESULT 5
Q03481 PRELIMINARY; PRT; 511 AA.
AC Q03481;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Alpha8 subunit of nicotinic acetylcholine receptor precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=90315158; PubMed=2369519;
RA Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
RT "Brain alpha-bungarotoxin-binding protein cDNAs and mABs reveal
RT subtypes of this branch of the ligand-gated ion channel gene
RT superfamily.";

```

RL Neuron 5:35-48(1990).
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 DR EMBL: X52296; CA336544.1; --
 DR PIR: JH0173; JH0173.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0005230; F: extracellular ligand-gated ion channel activity; IEA.
 DR GO: GO:0005216; F: ion channel activity; IEA.
 DR GO: GO:0030594; F: neurotransmitter receptor activity; IEA.
 DR GO: GO:0006811; P: ion transport; IEA.
 DR GO: GO:0007268; P: synaptic transmission; IEA.
 DR InterPro: IPR006201; Neur chan channel.
 DR InterPro: IPR006202; Neur chan LBD.
 DR InterPro: IPR006029; Neur channel memb.
 DR Pfam: PF02931; Neur chan LBD; 1. --
 DR Pfam: PF02932; Neur chan memb; 1.
 DR PRINTS: PR00252; NR1ONCHANNEL.
 DR TIGSFams: TIGR00860; LIC; 1.
 DR PROSITE: PS00236; NEUROTR ION CHANNEL; 1.
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
 KW Transmembrane.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 511 POTENTIAL.
 SQ SEQUENCE 511 AA; 58705 MW; 10F362D153EC87A7 CRC64;
 Query Match 67.4%; Score 1820.5; DB 13; Length 511;
 Best Local Similarity 69.0%; Pred. No. 5.4e-153;
 Matches 343; Conservative 56; Mismatches 93; Indels 5; Gaps 4;
 QY 8 VMLAASLLHYSLOGEFORKLYKELVKNYPLRPVANDSQPLTYFSLSLQIMDVDE 67
 Db 16 LNASLFLSPFKVSQSGSQRRLYDLRLNRYNLERPWNDSQFVVELQLSLQIDVDE 75
 QY 68 KQVLTNTNLQMSWDHYLQWNVSEYPGVKTRPDPDQIWKPDILLYNSADERDATH 127
 Db 76 KQVLTITNWLQWYVDIYLSWDQYEPGVQNLRFPSDQIWPDIILYNSADERDATH 135
 QY 128 TNLVNSSGHCQYLPGIPFKSSCYIDVRWFPDPVQHCCLKFGWSYSGWSLQMQEADI 187
 Db 136 TNLVNYSGSCQYIPPGILKSTCYIDVRWFPDPVQHCCLKFGSWTHSGWLIBQMLEADI 195
 QY 188 SGVINGEWDLVGIPKRSERFECKEYPDPVTFTVTRRTLYYGLNLLIPCVLISAL 247
 Db 196 SNIISGEWDLVGVPKRNELTYECKEYPDPVTFTVTRRTLYYGLNLLIPCVLISGL 255
 QY 248 ALLVFLPADSGEKISLGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFASTMIIVGLS 307
 Db 256 ALLVFLPADSGEKISLGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFASTMIIVGLS 315
 QY 308 VVVTVIVLQYHHDDGGKMPKWRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRC 364
 Db 316 VVVTVIVLQYHHDDPQAGKMPKWRVILLNWCWFLRMKRPGEN-IKPLSCKSYSPKHP 374
 QY 365 SLASVEMSAVAPPASGNLLYIGRGLDGVHCVPDPDSGVVCGRMACSPHDEHLHGG 424
 Db 375 SLKNTENVLPQHSNGNMIY-SYHTMENPCQNDLGSKGKICPLSDENHEVQKK 433
 QY 425 QPGEQDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFVSFTIICIT 484
 Db 434 ALMDTIPVIVKILEEVQYIARFRQDSEAVCSWKFAACVVDRLCLVAFTLAICTF 493
 QY 485 GILMSAPNFEAVSKDF 501
 Db 494 TILMSAPNFEAVSKDF 510
 RESULT 6
 QYT2S0
 ID QYT2S0 PRELIMINARY; PRT; 486 AA.
 AC QYT2S0;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Nicotinic acetylcholine receptor alpha 8a subunit (Fragment).
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 ON NCBI_TaxID=31033;
 RN [1]_SEQUENCE FROM N.A.
 RP Jones A.K., Elgar G., Sattelle D.B.;
 RA "The nicotinic acetylcholine receptor gene family of the pufferfish,
 RT Fugu rubripes";
 RL Genomics 0:0-0(2003).
 DR EMBL: AY299465; AAP59380.1; --
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 486 AA; 54942 MW; D27198395A87A4DA CRC64;
 Query Match 65.5%; Score 1769.5; DB 13; Length 486;
 Best Local Similarity 68.6%; Pred. No. 1.7e-148;
 Matches 338; Conservative 48; Mismatches 82; Indels 25; Gaps 6;
 QY 23 GEFORKLYKELVKNYPLRPVANDSQPLTYFSLSLQIMDVDEKQVLTNTNLQMSW 82
 Db 4 GPFORKLYHDLMVNYNRLERPVINDSAPIVVELGFTLQIIVDEKQVLTNTNLQMSW 63
 QY 83 TDHYLQWNVSEYPGVKTRPDPDQIWKPDILLYNSADERDATHFNTLVNSSGHCQYLP 142
 Db 64 TDYLSWNPESFPQVQNLRFPSLLIMPDILLYNSADERDATHFNTLVNATGVCQYIP 123
 QY 143 PGIFKSSCYIDVRWFPDPVQHCCLKFGWSYSGWSLQMQEADISGYPNGEWDLVGP 202
 Db 124 PGILKSTCYIDVRWFPDPVQHCCLKFGSWTHSGWLIBQMLEADI 183
 QY 203 GKRSERFECKEYPDPVTFTVTRRTLYYGLNLLIPCVLISALALLVFLPADSGEKI 262
 Db 184 AKRNELYDYCKEYPDPVTFTVTRRTLYYGLNLLIPCVLISGLALLVFLPADSGEKI 243
 QY 263 SLGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFASTMIIVGLSVTVVLQYHHDDP 322
 Db 244 SLGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFASTMIIVGLSVTVVLQYHHDDP 303
 QY 323 DGGKMPKWRVILLNWCWFLRMKRPGEKVRPAC-----QHKQRCSLASVEMSAV 374
 Db 304 HGGKMPKWRVILLNWCWFLRMKRPGEKQVASSRPPDHKRSPPHASSASTIQVATI 363
 QY 375 ---APPPASGNL-LYIGFR--GLDGVHCVPDPDSGVVCGRMACSPHDEHLHGGQPP 428
 Db 364 PQAPAPTANGNMLYFSYHALADNPTLPASDPVSIRSRQTRS-----LL-----LE 412
 QY 429 GDPDLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFVSFTIICITILM 488
 Db 413 QLPEISQILEEVQYIARFRQDSEAVCSWKFAACVVDRLCLVAFTLAICTF 472
 QY 489 SAPNFEAVSKDF 501
 Db 473 SAPNFEAVSKDF 485
 RESULT 7
 QYT2U0
 ID QYT2U0 PRELIMINARY; PRT; 555 AA.
 AC QYT2U0;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nicotinic acetylcholine receptor alpha 7b subunit (Fragment).
 GN A7B.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.

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OX NCBI_TaxID=31033;
RN
RP SEQUENCE FROM N.A.
RA Jones A.K., Elgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
RL Fugu rubripes.";
RT Genomics 0:0-0(2003).
DR EMBL; AY298752; AAP57216.1; -.
KW Receptor.
FT NON TER
SQ SEQUENCE 555 AA; 61010 MW; B042A3E4430A2B7C CRC64;

Query Match
Best Local Similarity 64.2%; Score 1734; DB 13; Length 555;
Matches 337; Conservative 52; Mismatches 93; Indels 72; Gaps 6;

QY 20 SLOQEFORGLYKELVKNYNPLERVANDSPLTVFSLQIQMDVDEKNOVLTNTWLQ 79
Db 1 SLOQPHQRTLLKLLKDYNERMERVANDSPLTVFSLQIQMDVDEKNOVLTNTWL 60
QY 80 MSWTDHYLQNVSEYPGVKTVPDQGIWKPDILLNSADDERFDTFTNVLNNSGHQ 139
Db 61 MSWFDHYLQNVSEYPGVKNLRFPTDQIWTDPDILLNSADDDFDSTFTKNVLNNS 120
QY 140 YLPPIGFKSSCYDVRPFDDVQCKLKFGSWYGGWSLDLQMRADISGYIPNGEWD 199
Db 121 YQPPGIFMSTCNDVRPFDDIQRCELKFGSWYDGLLDLQMNREADISGYMANGEW 180
QY 200 GIFKRSERFECCKEYPDVFTVMTRRRTLYYGLNLLIPCVLISALALLVFL 259
Db 181 GVPGRNEVFYDCKEYPATVFAIRRTLYYALNLLIPCVLLSSNTLLIFVLPAD 240
QY 260 EKISLGLTIVLSLTVFMLVAEIMPATSDSVPLIAQYFASMTIIVGLSVVTV 319
Db 241 EKISLGLTIVLSLTVFMLVAEIMPATSDSVPLIGYFASIMIIVGMSVATV 300
QY 320 HDPDGGKMPKWTVRILLNCAWFLMKRPGCE--DKVTPACQHKORRCSLASEM 377
Db 301 HDPNGMMPKVVQLVQLQWAVFLMKRPGCEKSPERPCCAPHLRCSGSGS 360
QY 378 -----PASNGNLLYIGFRLDGVHCVPTP--DS 403
Db 361 DHALHPLHPQGLAPLQPGGLHAGOPHYHAQSSANNNGNLVILGFQSVDSAG 420
QY 404 GVVCG--RMACS-PTHDEHLLHGGQPEE----- 428
Db 421 NISTGPPRVAGSPPHLPQFCSPSPPPASNMMDTGPCSTVSSGGGFGGGGLG 480
QY 429 -GPDPLAKILLEEVRYIANRFRCDSEAVSEWKFACVVDRLCLMAFSVFTII 487
Db 481 VGDPLHALLLEEVRFVADRFREQDEVSQAADQWKFAVIDRLCLNAFSVFTII 540
QY 488 MSAPNFVEAVSKDF 501
Db 541 MSAPNFVEALSKDF 554

RESULT 8
Q8IU24 PRELIMINARY; PRT; 321 AA.
AC Q8IU24;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;

Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC037571; AAH37571.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti.; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMs; TIGR00860; LiC; 1.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 35481 MW; 2998C11DD1F15A89 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e-143;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 182 MQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVMTRRRTLYYGLNLL 241
Db 1 MQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVMTRRRTLYYGLNLL 60
QY 242 VLISALALLVFLPADSGEKISLGIITVLLSLTVFMLVAEIMPATSDSVPLIAQ 301
Db 61 VLISALALLVFLPADSGEKISLGIITVLLSLTVFMLVAEIMPATSDSVPLIAQ 120
QY 302 IIVGLSVVTVVIVLQVHHDDPGCKMPKWTVRILLNCAWFLMKRPGEDKVPAC 361
Db 121 IIVGLSVVTVVIVLQVHHDDPGCKMPKWTVRILLNCAWFLMKRPGEDKVPAC 180
QY 362 RRCSLASVMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGMACSPTHD 421
Db 181 RRCSLASVMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGMACSPTHD 240
QY 422 HGOQPEGDDPLAKILLEEVRYIANRFRCDSEAVSEWKFACVVDRLCLMAFSV 481
Db 241 HGOQPEGDDPLAKILLEEVRYIANRFRCDSEAVSEWKFACVVDRLCLMAFSV 300
QY 482 CTIGILMSAPNFVEAVSKDPA 502
Db 301 CTIGILMSAPNFVEAVSKDPA 321

RESULT 9
Q7T2T9 PRELIMINARY; PRT; 554 AA.
AC Q7T2T9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 7c subunit (Fragment).
GN A7C.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN
RP SEQUENCE FROM N.A.
RA Jones A.K., Elgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
RL Fugu rubripes.";
RT Genomics 0:0-0(2003).
DR EMBL; AY298753; AAP57217.1; -.
KW Receptor.
FT NON TER
SQ SEQUENCE 554 AA; 61565 MW; 8C46BCC6B20B5AFB CRC64;

Query Match
Best Local Similarity 58.3%; Score 1575.5; DB 13; Length 554;
Matches 309; Conservative 55.7%; Pred. No. 3.5e-131;
Matches 309; Conservative 68; Mismatches 103; Indels 75; Gaps 8;

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QY 20 SLOGEFQKLYKELVKNYNPLERPVANDSOPLTIVYFSLSLQIQMDVDEKQVLTINWLQ 79
Db 1 SVQGPQORFELLTELLKDYNEPWPVANDSQAALTQFSFILIQMDVDEKQVLTINWLQ 60
QY 80 MSWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLYNSADERPDATFHTNVLVNSGHCQ 139
Db 61 MOWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLYNSADERPDATFHTNVLVNSGHCQ 120
QY 140 YLPPGIFKSCYIDVNFPPDVQHCCKLFGSGWSYGLDQMOEADISGYIENGWDLV 199
Db 121 YLPPGIFKSCYIDVNFPPDVQHCCKLFGSGWSYGLDQMOEADISGYIENGWDLV 180
QY 200 GIFKGSERYECKEYPPDVTFVTVMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 259
Db 181 EVPGGRHEVYDCABEYPPDVTFVTVMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 240
QY 260 EKISLGIITVLLSVTVMMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIYQYH 319
Db 241 EKISLGIITVLLSVTVMMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIYQYH 300
QY 320 HDPDGGKMPKTRVILLNWCWFLRMKRPGEOKVRPACQHKQ-----RRCS-----LASVE 370
Db 301 HNTNNGOMPRWHLVLLQWIPFLRMKHPGETB-EPSLPHSQTSASORKLSSPGTSSSS 359
QY 371 MSNAVAPPPAS-----NGMLLYIGFRGLDGVHCVTPDPSGVVCGRMAC- 412
Db 360 SSSAAARPANTDQGLSLRQHQSLNGALYVGFQATAPR-LPQRSRSVNGRVGCG 418
QY 413 -----SPTHDEHLL-----HGG--QP 426
Db 419 DGEAGASVREGPSLVQRLPLSLKSEVPQLEGTPGPDASSGSGAEPHPGGLTQS 478
QY 427 PEGDPLAKILEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIGI 486
Db 479 FVVRRLQALLAEVQFLVERVKQDRQLRLAEQWQFAASVIDRLFLVGSVFNICTIAI 538
QY 487 LMSAPNFVAVSKDF 501
Db 539 LMAAPHFGALSXDF 553

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RESULT 10

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Q7T2U1 ID Q7T2U1 PRELIMINARY; PRT; 474 AA.
AC Q7T2U1;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 7a subunit (Fragment).
GN A7A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]_TaxID=31033;
RP SEQUENCE FROM N.A.
RA Jones A.K., Elgar G., Sattelle D.B.;
RT "The nicotinic acetylcholine receptor gene family of the pufferfish,
RT Fugu rubripes."
RL Genomics 0:0-0(2003).
DR EMBL; AY298751; AAP57215.1; -.
KW Receptor.
FT NON TER
SQ SEQUENCE 474 AA; 53180 MW; 9843B897C8D505FD CRC64;

```

Query Match 58.1%; Score 1569.5; DB 13; Length 474;
 Best Local Similarity 63.1%; Pred. No. 9.6e-131;
 Matches 306; Conservative 64; Mismatches 100; Indels 15; Gaps 5;

QY 20 SLOGEFQKLYKELVKNYNPLERPVANDSOPLTIVYFSLSLQIQMDVDEKQVLTINWLQ 79

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Db 1 TVQGPTEERLYNLLRYNSMIRPVANDSETLMVRLGLSLQIMDVDEKQVLTINWLQ 60
QY 80 MSWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLYNSADERPDATFHTNVLVNSGHCQ 139
Db 61 MOWTDHYLQWNVSEYFGVKTVPDPGQIWKPDILLYNSADERPDATFHTNVLVNSGHCQ 120
QY 140 YLPPGIFKSCYIDVNFPPDVQHCCKLFGSGWSYGLDQMOEADISGYIENGWDLV 199
Db 121 YLPPGIFKSCYIDVNFPPDVQHCCKLFGSGWSYGLDQMOEADISGYIENGWDLV 180
QY 200 GIFKGSERYECKEYPPDVTFVTVMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 259
Db 181 EVPGGRHEVYDCABEYPPDVTFVTVMRRRTLYYGLNLLIPCVLISALALLVFLPADSG 240
QY 260 EKISLGIITVLLSVTVMMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIYQYH 319
Db 241 EKISLGIITVLLSVTVMMLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVIYQYH 300
QY 320 HDPDGGKMPKTRVILLNWCWFLRMKRPGEOKVRPACQHKQ-----RRCS-----LASVE 379
Db 301 HDPDGGKMPKTRVILLNWCWFLRMKRPGEOKVRPACQHKQ-----RRCS-----LASVE 359
QY 380 SGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPHDEHLLHGGQPPGEG---DPLAKI 436
Db 360 PTN--VYPSISGLKS-----SQTTPVPGGRAG---EDELAKAGPGSSAGNIERELAKL 408
QY 437 LEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIGIILMSAPNFVAV 496
Db 409 LEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIGIILMSAPNFVAV 468
QY 497 VSKDF 501
Db 469 FSKNF 473

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RESULT 11

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Q86MN7 ID Q86MN7 PRELIMINARY; PRT; 542 AA.
AC Q86MN7;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Nicotinic acetylcholine receptor subunit Dalpha7 precursor.
GN NACRALPHA-18C.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP SEQUENCE FROM N.A.
RA Millar N.S.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ554210; CAD86936.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti...; IEA.
DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Signal; Receptor.
FT SIGNAL
FT CHAIN 36 542
FT SEQUENCE 542 AA; 60988 MW; 69D2C39746BB74D7 CRC64;

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Query Match 47.0%; Score 1271; DB 5; Length 542;
Best Local Similarity 46.8%; Pred. No. 3.8e-103;
Matches 252; Conservative 87; Mismatches 133; Indels 66; Gaps 8;

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QY 6 GGVWALAAALL---HVSLOQEFORFKYKLVKNVPLERPVANDSQPLTVYESLSLQI 62
DB 16 GGRMLVYGLGLIMIPACAGPHEKRLHALLDNVNSLPRVNESDPLQFSLTLMQI 75
QY 63 MDVDEKQVLTNTIWLQMSWTDHYLQNVNSYPYGVKTVPFDDGQIWKPDILLNSADERY 122
DB 76 IDVDKQQLITNTIWLKLEWMDMLRWNSEFGVGRDLRIIPHLKPKDVLWNSADEGF 135
QY 123 DATHTNTVNVNSGHCQVLPKIKSSCYIDVRFPDVOQCKLFGKFSWVGWSLIDQM 182
DB 136 DGTATNVNVNNSGSLVPPGIFKSTCKIDITWFPDDQRCCKMFKGTSWTYDGFQDLQL 195
QY 183 QE---ADISGYIPNGEWDLVGIPGKRSEFYECCKEPEVDVFTVWRRRTLYYGLNLI 239
DB 196 QDEAGGDISSFITNGEWDLVGPKRNEIYVNCPEYIDITFAILLRKLTYFFNLIIV 255
QY 240 PCVLISALALVFLPADSGKISIGITVLSLTFVLMVAEIMPATSDSVPLIAQYFAS 299
DB 256 PCVLIASMALLGFTLPDPSGKLSIGVTLISLTFVLMVAETPATSDAVPLILGKYFNC 315
QY 300 TMIIVGLSVVTVLVLYVHHDDPGKMPKTRVILLNWCANFLMKRPG----- 349
DB 316 IMFVASSVSTILVLYHNRNPDTHSEWIRVIFLYLPICILRMQRPQGVYECPPPP 375
QY 350 -----EKKVPA-----COHQKRCSLASVMSAVAP 376
DB 376 SSSSSASGKKQIQNVELKERSKSLANLVLDIDDDFCNH---RCA-----SATLP 426
QY 377 PPASNGNLLYIGFGLDGVHCVPPTDGSVGVGRMACSPTDHEHLHGGQPEGDPDLAKI 436
DB 427 HQPTYRTMY---RQGDGSGVPGVPGVVDGRL-----HEATSHCLTSSABVELALI 478
QY 437 LEEVRYIANPRCDSEAEVSEWKEACVVDRLCLMAFSVFTTICITIGILMSAPNV 494
DB 479 LKELRWTEQLKKEDETSIDTRDKFAAMVVDRLCLIFTLTITLTIATLAVLFSAPHF 536
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RESULT 12

```
Q9VW19 PRELIMINARY; PRT; 545 AA.
AC Q9VW19;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG32538 protein.
GN NACR-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.N., Bouck J., Brokstein P., Brotter P.,
RA Burtova K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RL "Annotation of Drosophila melanogaster genome."
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003511; AAF48950.2; -.
DR FlyBase; FBgn0031014; nACR-alpha-18C.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0005230; F.extracellular ligand-gated ion channel acti. .; IEA.
DR GO; GO:0030594; F.neurotransmitter receptor activity; IEA.
DR GO; GO:0006811; P.ion transport; IEA.
DR InterPro; IPR006201; Neur channel.
DR InterPro; IPR006202; Neur chan IBD.
DR InterPro; IPR006029; Neu_chan_LED_1_memb.
DR Pfam; PF02931; Neur_chan_LED_1_memb.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
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Wed May 12 09:51:15 2004

us-09-703-951a-12.rsp

Page 10

Db 453 DADISRDWKEAMVDRCLLIIFTLETTIATLAVLSAPHIM 494

Search completed: May 5, 2004, 15:31:29
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:27:53 ; Search time 21 Seconds
(without alignments)
2299.436 Million cell updates/sec

Title: US-09-703-951a-12
Perfect score: 2702
Sequence: 1 MRCSPGGVWLAASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2694	99.7	502	1	ACHUA7
2	2694	99.7	502	2	nicotinic acetylch alpha 7 neuronal n
3	2549	94.3	502	2	nicotinic acetylch
4	2535	93.8	502	2	nicotinic receptor
5	2433	90.0	502	2	nicotinic acetylch
6	1820.5	67.4	511	2	alpha-bungarotoxin
7	1108.5	41.0	498	2	nicotinic acetylch
8	1093.5	40.5	560	2	hypothetical prote
9	999	37.0	461	2	hypothetical prote
10	949	35.1	557	2	nicotinic acetylch
11	946.5	35.0	511	2	nicotinic acetylch
12	945	35.0	542	2	hypothetical prote
13	942.5	34.8	459	2	nicotinic acetylch
14	941.5	34.8	528	1	ACHCH2N
15	940.5	34.8	503	2	nicotinic acetylch
16	938	34.7	622	1	ACCH4N
17	937.5	34.7	576	1	ACRFA2
18	937	34.7	502	2	nicotinic acetylch
19	926	34.3	567	1	ACRFA1
20	920	34.0	627	2	JC4021
21	919.5	34.0	495	2	S60589
22	917.5	34.0	625	2	A26456
23	913	33.8	495	2	B35721
24	902	33.4	494	2	T09289
25	896	33.2	517	2	A30992
26	891.5	33.0	499	2	A24572
27	885	32.8	498	2	G02421
28	881	32.6	521	1	ACFFNN
29	880.5	32.6	491	1	ACCHNN

ALIGNMENTS

RESULT 1

ACHUA7

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N;Alternate names: cholinergic nicotinate receptor alpha-7 chain
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 22-Jun-1999
C;Accession: I37185; A54194; S60309
R;Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.
Mol. Pharmacol. 45, 546-554, 1994
A;Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the omers expressed in Xenopus oocytes.
A;Reference number: I37185; MUID:94195283; PMID:8145738
A;Accession: I37185

A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-502 <PEN>

A;Cross-references: EMBL:X70297; NID:g496606; PIDN:CAA49778.1; PID:g496607
A;Experimental source: brain neuroblastoma cell line SHSY-5Y
R;Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaret, M.; Heinemann, S.
Genomics 19, 379-381, 1994
A;Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotinic
A;Reference number: A54194; MUID:94245214; PMID:8188270
A;Accession: A54194

A;Molecule type: mRNA
A;Residues: 24-363, 'S', '365-374, 'A', '376-408, 'AWPAP', 414-502 <CHI>
A;Cross-references: GB:Z23141; NID:g457736; PIDN:CAA80672.1; PID:g457737
A;Experimental source: retina

C;Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localiz
C;Genetics:
A;Gene: GDB:CHRNA7
A;Cross-references: GDB:138751; OMIM:118511
A;Map position: 15q14-15q14
A;Note: defects in this gene have been associated with mental retardation and schizop
C;Complex: the functional receptor molecule is a heteropentamer with two alpha chains
C;Superfamily: acetylcholine receptor

F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pre
F;231-254/Domain: transmembrane #status predicted <TR1>
F;262-280/Domain: transmembrane #status predicted <TR2>
F;296-317/Domain: transmembrane #status predicted <TR3>
F;470-488/Domain: transmembrane #status predicted <TR4>
F;46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;150-164/Disulfide bonds: #status predicted
F;365,413/Binding site: phosphate (Ser) (covalent) #status predicted
F;415/Binding site: phosphate (Thr) (covalent) #status predicted
F;442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 99.7%; Score 2694; DB 1; Length 502;

Best Local Similarity 99.6%; Pred. No. 1.7e-224; Indels 0; Gaps 0;
Matches 500; Conservative 0; Mismatches 2;

QY 1 MRCSPGGVWLAALASLLHVSLLQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLIL 60
 DB 1 MRCSPGGVWLAALASLLHVSLLQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLIL 60
 QY 61 QIMDVDEKNOVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADE 120
 DB 61 QIMDVDEKNOVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADE 120
 QY 121 RFDAFHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFDVQCHCKLKFGSWSYGGWSL 180
 DB 121 RFDAFHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFDVQCHCKLKFGSWSYGGWSL 180
 QY 181 QMQRADISGYIPNGEWDLVGIFPKRSERYECCKEPYDVTVTVMRRRTLYYGLNLLIP 240
 DB 181 QMQRADISGYIPNGEWDLVGIFPKRSERYECCKEPYDVTVTVMRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
 QY 361 QRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHL 420
 DB 361 QRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHL 420
 QY 421 LHGGOPPEGDPLAKILLEEVRYIANRFRQDESEAVCSWKFAACVDRLCIMAFSVFTI 480
 DB 421 LHGGOPPEGDPLAKILLEEVRYIANRFRQDESEAVCSWKFAACVDRLCIMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

G02259
 alpha 7 neuronal nicotinic acetylcholine receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1995 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
 C:Accession: G02259
 R:Leonard, S.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: H00936
 A:Accession: G02259
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-502 <LEO>
 A:Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
 C:Superfamily: acetylcholine receptor

Query Match 99.7%; Score 2694; DB 2; Length 502;
 Best Local Similarity 99.6%; Pred. No. 1.7e-224;
 Matches 500; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLLQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLIL 60
 DB 1 MRCSPGGVWLAALASLLHVSLLQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLIL 60
 QY 61 QIMDVDEKNOVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADE 120
 DB 61 QIMDVDEKNOVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADE 120
 QY 121 RFDAFHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFDVQCHCKLKFGSWSYGGWSL 180
 DB 121 RFDAFHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFDVQCHCKLKFGSWSYGGWSL 180
 QY 181 QMQRADISGYIPNGEWDLVGIFPKRSERYECCKEPYDVTVTVMRRRTLYYGLNLLIP 240
 DB 181 QMQRADISGYIPNGEWDLVGIFPKRSERYECCKEPYDVTVTVMRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
 QY 361 QRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHL 420
 DB 361 QRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHL 420
 QY 421 LHGGOPPEGDPLAKILLEEVRYIANRFRQDESEAVCSWKFAACVDRLCIMAFSVFTI 480
 DB 421 LHGGOPPEGDPLAKILLEEVRYIANRFRQDESEAVCSWKFAACVDRLCIMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
 A57175
 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
 C:Accession: A57175
 R:Ort-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
 Genomics 26, 399-402, 1995
 A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine rec
 A:Reference number: A57175; MUID:95324936; PMID:7601470
 A:Accession: A57175
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-502 <ORR>
 A:Cross-references: GB:L37663; NID:g790853; PIDN:AAC42053.1; PID:g790854
 C:Superfamily: acetylcholine receptor
 C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprote
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
 F:231-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:46.90.133/Binding site: carbohydrate (Aen) (covalent) #status predicted
 F:365.413.427/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 94.3%; Score 2549; DB 2; Length 502;
 Best Local Similarity 94.0%; Pred. No. 5.5e-212;
 Matches 467; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

QY 6 GGVWLAALASLLHVSLLQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLILQIMDV 65
 DB 6 GGVWLAALASLLHVSLLQGEFORKLYKELVKYNPLERPVANDSQPLTVYFSLILQIMDV 65
 QY 66 DEKNQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADERFAT 125
 DB 66 DEKNQVLTNTIWLQMSWTDHYLQWNVSEYGVKTVRPDQGIWKPDIILLNSADERFAT 125
 QY 126 FHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFDVQCHCKLKFGSWSYGGWSLQMOEA 185
 DB 126 FHTNVLVNSGHCQYLPPGIFKSSCYIDVRWFFDVQCHCKLKFGSWSYGGWSLQMOEA 185
 QY 186 DISGYIPNGEWDLVGIFPKRSERYECCKEPYDVTVTVMRRRTLYYGLNLLIPCVLIS 245
 DB 186 DISGYIPNGEWDLVGIFPKRSERYECCKEPYDVTVTVMRRRTLYYGLNLLIPCVLIS 245
 QY 246 ALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
 DB 246 ALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305

QY 306 LSVVTVTVLVQHHDDPGGKMPKWTTRVILLNWCAMFLRMKRPGEKVPACQHKQRCS 365
DB 306 LSVVTVTVLVVYHHDDPGGKMPKWTTRVILLNWCAMFLRMKRPGEKVPACQHKPRCS 365
QY 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVCHVCTPTDPSGVVCGMACSPTHDEHLHGQ 425
DB 366 LASVELSAGAPPTSNGNLLYIGFRGLEGMHCAPTDSGVVCGRLACSPTHDEHLMHGTH 425
QY 426 PPEGDDPLAKILEEVRYIANRFRCDSEAVCSSEKFAACVVDRLCLMAFVSFTIICITG 485
DB 426 PSDGDDPLAKILEEVRYIANRFRCDSEVICSEKFAACVVDRLCLMAFVSFTIICITG 485
QY 486 ILMSAPNFVEAVSKOFA 502
DB 486 ILMSAPNFVEAVSKOFA 502

RESULT 4
T01378
nicotinic receptor alpha 7 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01378
R;Seguella, P.; Madiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A:Title: Molecular cloning, functional properties, and distribution of rat brain alpha 7
A:Reference number: Z14310; MUID:93147931; PMID:7678857
A:Accession: T01378
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <SEG>
A:Cross-references: EMBL:S53987; NID:g264770; PIDN:AA25224.2; PID:g5705903
A:Experimental source: brain
A:Superfamily: acetylcholine receptor

Query Match 93.8%; Score 2535; DB 2; Length 502;
Best Local Similarity 93.6%; Pred. No. 9e-211;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 6 GGVLALAAALLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLQLQIMDV 65
DB 6 GGVLALAAALLHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLQLQIMDV 65
QY 66 DERNOVLTTNIWLQMSWTDHYLQMVSEYFGVKTVRFPDQGIWKPDILLNSADERFDT 125
DB 66 DERNOVLTTNIWLQMSWTDHYLQMVSEYFGVKTVRFPDQGIWKPDILLNSADERFDT 125
QY 126 FHTNVLNNSGHCQYLPPIGIFKSSCYIDVRFPDVOHQCKLFGSWSYGGMSLDLQMOEA 185
DB 126 FHTNVLNNSGHCQYLPPIGIFKSSCYIDVRFPDVOHQCKLFGSWSYGGMSLDLQMOEA 185
QY 186 DISGYIPNGEWDLVGIPGKSEREYECCKEPYDVTVTVMRRRLYYGLNLLIPCVLIS 245
DB 186 DISGYIPNGEWDLVGIPGKSEREYECCKEPYDVTVTVMRRRLYYGLNLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLGTIVLLSTVFMLLVAEIMPATSDSVPLIAQYFASFTMIIVG 305
DB 246 ALALLVFLPADSGEKISLGTIVLLSTVFMLLVAEIMPATSDSVPLIAQYFASFTMIIVG 305
QY 306 LSVVTVTVLVQHHDDPGGKMPKWTTRVILLNWCAMFLRMKRPGEKVPACQHKQRCS 365
DB 306 LSVVTVTVLVVYHHDDPGGKMPKWTTRVILLNWCAMFLRMKRPGEKVPACQHKPRCS 365
QY 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVCHVCTPTDPSGVVCGMACSPTHDEHLHGQ 425
DB 366 LASVELSAGAPPTSNGNLLYIGFRGLEGMHCAPTDSGVVCGRLACSPTHDEHLMHGTH 425
QY 426 PPEGDDPLAKILEEVRYIANRFRCDSEAVCSSEKFAACVVDRLCLMAFVSFTIICITG 485
DB 426 PSDGDDPLAKILEEVRYIANRFRCDSEVICSEKFAACVVDRLCLMAFVSFTIICITG 485
QY 486 ILMSAPNFVEAVSKOFA 502
DB 486 ILMSAPNFVEAVSKOFA 502

DB 486 ILMSAPNFVEAVSKOFA 502

RESULT 5
JN0113
nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
N:Alternate names: alpha-bungarotoxin-binding protein alpha chain
C:Species: Gallus gallus (Chicken)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
C:Accession: JN0113; JH0172; S28018; B25738; S26566
R;Coururier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.
Neuron 5, 847-856, 1990
A:Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmenta
A:Reference number: JN0113; MUID:91097796; PMID:1702646
A:Accession: JN0113
A:Molecule type: DNA
A:Residues: 1-502 <CON>
A:Cross-references: GB:X68586; NID:g287756; PIDN:CAA48576.1; PID:g287757
A:Experimental source: white leghorn; brain
R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAb reveal subtypes of th
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0172
A:Molecule type: mRNA
A:Residues: 1-18 <MAS>
A:Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
A:Experimental source: white leghorn; erythrocyte
R;Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; J
Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
A:Title: Brain and muscle nicotinic acetylcholine receptors are different but homologou
A:Reference number: A94055; MUID:85270494; PMID:3860855
A:Accession: B25738
A:Molecule type: protein
A:Residues: 24-25, 27, 28-41, X', 43-45, X', 47 <CON>
C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localiz
C:Genetics:
A:Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotei
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pre
F;231-254/Domain: transmembrane #status predicted <TR1>
F;262-280/Domain: transmembrane #status predicted <TR2>
F;296-317/Domain: transmembrane #status predicted <TR3>
F;470-488/Domain: transmembrane #status predicted <TR4>
F;46,90,133/Binding site: carboxydrate (Asn) (covalent) #status predicted
F;365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted
F;415/Binding site: phosphate (Thr) (covalent) #status predicted
F;442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 90.0%; Score 2433; DB 2; Length 502;
Best Local Similarity 90.3%; Pred. No. 5.7e-202;
Matches 450; Conservative 18; Mismatches 27; Indels 0; Gaps 0;

QY 8 VTLAAALHVSLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLQLQIMDVDE 67
DB 8 LMLAAGLVRESLSQGEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLQLQIMDVDE 67
QY 68 KNOVLTTNIWLQMSWTDHYLQMVSEYFGVKTVRFPDQGIWKPDILLNSADERFDTFH 127
DB 68 KNOVLTTNIWLQMSWTDHYLQMVSEYFGVKTVRFPDQGIWKPDILLNSADERFDTFH 127
QY 128 TTNVLNNSGHCQYLPPIGIFKSSCYIDVRFPDVOHQCKLFGSWSYGGMSLDLQMOEADI 187


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Db      128  TNVLNNSGHCOYLPGLFKSSCYIDVWFFDVQKNLKFSGWTYGGWSDLLQOEADI 187
QY      188  SGYIPNGEWDLVIGPKSERFYECKEYPDPVTFVTMRRRTLYYGLNLLIPCVLISAL 247
Db      188  SGYIPNGEWDLVIGPKSERFYECKEYPDPVTFVTMRRRTLYYGLNLLIPCVLISAL 247
QY      248  ALLVFLPADSGEKISLGITVLLSLTFVMLVAETMPATSDSVPLIAQYFASIMVIGLS 307
Db      248  ALLVFLPADSGEKISLGITVLLSLTFVMLVAETMPATSDSVPLIAQYFASIMVIGLS 307
QY      308  VVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHKQRCSLA 367
Db      308  VVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHKQRCSLS 367
QY      368  SVMSAVAPPASNGNLIYIGRGLDGVCVPTDPDGVVCGRMACSPHDEHLLGGQPP 427
Db      368  SVMSAVAPPASNGNLIYIGRGLDGVCVPTDPDGVVCGRMACSPHDEHLLGGQPP 427
QY      428  EGDPLAKLIEVRVIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIGIL 487
Db      428  EGDPLAKLIEVRVIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIGIL 487
QY      488  MSAPNFVEAVSKDFA 502
Db      488  MSAPNFVEAVSKDFA 502

RESULT 6
JH0173
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MABs reveal subtypes of this
A:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
C:Accession: JH0173
R:Schaeffer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0173
A:Molecule type: mRNA
A:Cross-references: GB:X52296; NID:G63081; PIDN:CAA3544.1; PID:G63082
A:Experimental source: brain
A:Note: This sequence is similar to acetylcholine receptor alpha chains
C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <AH
F:239-262/Domain: transmembrane #status predicted <TM1>
F:270-288/Domain: transmembrane #status predicted <TM2>
F:304-323/Domain: transmembrane #status predicted <TM3>
F:479-496/Domain: transmembrane #status predicted <TM4>
F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      67.4%; Score 1820.5; DB 2; Length 511;
Best Local Similarity 69.0%; Pred. No. 4.4e-149;
Matches 343; Conservative 56; Mismatches 93; Indels 5; Gaps 4;

QY      8  VMLAASLLHVSQGEFQRLKYLKVNYNPLERPVANDSQPLTYVFSLLQIMDVDE 67
Db      16  LMASLFLSFVKVQSQRRLYDLRNLYRNLERPVANDSQPIVVELQLSLQIIDVDE 75
QY      68  KNOVLTTNIWQSWTDHYLQWNVSEYPGVKTVRPDQGIWKPDILLNYSADRFDATFH 127
Db      76  KNOVLITNWLQWYWDIYLSWQYEPGVQGNURFSDQIWKPDILLNYSADRFDATFH 135
QY      128  TNVLNNSGHCOYLPGLFKSSCYIDVWFFDVQHKCLKFGSWSGWSDLLQOEADI 187
Db      136  TNVLNNSGHCOYLPGLFKSSCYIDVWFFDVQHKCLKFGSWSGWSDLLQOEADI 195
QY      188  SGYIPNGEWDLVIGPKSERFYECKEYPDPVTFVTMRRRTLYYGLNLLIPCVLISAL 247

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Db      196  SNYISNGEWDLVGPVKRKNELYECCKEYPDPVTFVTMRRRTLYYGLNLLIPCVLISGL 255
QY      248  ALLVFLPADSGEKISLGITVLLSLTFVMLVAETMPATSDSVPLIAQYFASIMVIGLS 307
Db      256  ALLVFLPADSGEKISLGITVLLSLTFVMLVAETMPATSDSVPLIAQYFASIMVIGLS 315
QY      308  VVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHK--QRRC 364
Db      316  VVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHK--QRRC 374
QY      365  SLASVMSAVAPPASNGNLIYIGRGLDGVCVPTDPDGVVCGRMACSPHDEHLLGG 424
Db      375  SLKNTNVLFGHOPSGNMIY-SYHTMENPCCQNNDLGSKGKITCPLSEDEHVKQK 433
QY      425  QPPSGDPLAKLIEVRVIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICTI 484
Db      434  ALMDTIPVIVKLEEVQFIAMRFKQDEGEICSEWKPAAVADRCLCLVAFTLAICTFF 493
QY      485  GILMSAPNFVEAVSKDF 501
Db      494  TILMSAPNFIEAVSKDF 510

RESULT 7
S68588
A:Title: Nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis
A:Species: Caenorhabditis elegans
C:Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999
C:Accession: S68588; S57496
R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.
J. Mol. Biol. 258, 261-269, 1996
A:Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.
A:Reference number: S68587; MUID:96196478; PMID:8627624
A:Accession: S68588
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-498 <BAL>
A:Cross-references: EMBL:X83887; NID:G872087; PIDN:CAA58764.1; PID:G872088
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrar
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <M

Query Match      41.0%; Score 1108.5; DB 2; Length 498;
Best Local Similarity 44.6%; Pred. No. 1.3e-87;
Matches 226; Conservative 77; Mismatches 167; Indels 37; Gaps 7;

QY      10  LALAASLLHVSQGEFQRLKYLKVNYNPLERPVANDSQPLTYVFSLLQIMDVDEK 68
Db      6  LLISCAILAAAPTGLSLOERLYEDLRNLYRNLERPVANHSPEVTVHLKVALQOIIDVDEK 65
QY      69  NOVLTTNIWQSWTDHYLQWNVSEYPGVKTVRPDQGIWKPDILLNYSADRFDATFHT 128
Db      66  NOVTVNWLWLDYTNWYNLWMDKAYGNITDVRFPAGKIWKPDVLLNYSVDINFDSTYQT 125
QY      129  NVLNNSSGHCOYLPGLFKSSCYIDVWFFDVQHKCLKFGSWSGWSDLLQOEAD--D 186
Db      126  NMIVYSTGLVHWVPPGIFKISKIDIQWFFPEDEQCFKFGSWTYDGYKLIQATGGPD 185
QY      187  ISGYIPNGEWDLVIGPKSERFYECKEYPDPVTFVTMRRRTLYYGLNLLIPCVLISA 246
Db      186  ISEYISNGEWALPLTIVTERNEKFPYDCCPEYPDHFYIHRMRRTLYYGNLIMPICITL 245
QY      247  LALLVFLPADSGEKISLGITVLLSLTFVMLVAETMPATSDSVPLIAQYFASIMVIGL 306
Db      246  WTLGFTLPDAGEKITQITVLLSICFSLISVSEMSPTSEAVPLIGIFFCCMIVVTA 305
QY      307  VVVTVIVLQYHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHKQRCSL 366
Db      306  STVFTVYVNLNHYRTPETHDMGPTNRNLLLYVPIWILRMKRPG-----HNLTYASL 356
QY      367  ASVMSAVAPPASNGNLIYIGRGLDGVCVPTDPS-----GVVCGMAC 412

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Db 357 PSL-----FSTKPNRHSRLIRNIK--DNEHSLGRANSFDACRLNQYIMTQSVNGLTSL 410
QY 413 SPTHDEHLLHGGQPPEGDPD-----LAKILEEVRVYIANFRFCODESAVCSWKFAACVV 467
Db 411 GSTPSTWISSNGTTTDSQATLLILHRIYHEUKIVTKRMIEGDKKEQACNNKFAAMVV 470
QY 468 DRLCIMAFSVFTTICTIGILMSAPNFV 494
Db 471 DRLCXYVFTTIIIVSTIGIFWSAPYLV 497

RESULT 8
T19622
hypothetical protein C31H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T19622
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-560 <WIL>
A:Cross-references: EMBL:Z93778; PIDN: CAB07843.1; GSPDB: GN00019; CESP: C31H5.3
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP: C31H5.3
A:Map position: 1
A:Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C:Superfamily: acetylcholine receptor

Query Match 40.5%; Score 1093.5; DB 2; Length 560;
Best Local Similarity 40.8%; Pred. No. 2.9e-86;
Matches 227; Conservative 93; Mismatches 156; Indels 81; Gaps 9;

QY 10 LALAASLL-----HVSLOGEFORKLYKEIVKNYNPLERPVANDSOPLTIVFSLSLQI 62
Db 8 LVLSVILLIWEKCKSVITWGDHERRLYAKLAENYNKLARPVNESEAVVLLGMDYQOI 67
QY 63 MDVDEKQVLTNTLWQMSWDHVLQNVSEYPGVKTRFDPGQIWKPDILLYNSADERF 122
Db 68 LDIDKEHQIMNSNWLRSWTDHLYTWPDSFBNKEIVRLPINNIWKPDVLLYNSVDQOF 127
QY 123 DATFTNTLVNNSGHCOQLPGIFKSCYIDVRWPPDVQCHCKLFGSWSYGGNSLDQM 182
Db 128 DSTWPNVAVLYTGNVTWIPALIRSSCAIDIAFPFTQCTWKFSGSWTISGFTDLIN 187
QY 183 QEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVFTVMRRRTLYYGLMLIPCV 242
Db 188 TTISPATYKPNGEWELLGLTSQSRISFFYECCPEPYDVTFTVIRRTLYYGFNLLPCM 247
QY 243 LISALALVLLPADSGEKISIGITVLLSLTVMLLVAEIMPATSDSVPLIAQYFASWTMI 302
Db 248 LISSALLSFTLPADCGEKLNGVTFMSLCVFMVAEAMPQTSDAFLPIQIYFSCIMF 307
QY 303 IVGLSVVVTIVLYQVHHDDPGGK-MPKWTRVILLNWCAMFLMRKPGEDKVRPACQ-- 359
Db 308 QVGSVAVTATVIANFHRHSPEQYKPMKFKTLTLLGLMFTLLGMRPDLVLSVHGAYHA 367
QY 360 ----KQRCISLASVEMSAVAPPASNGNLLYIGFGLD----- 393
Db 368 SDNKKKQRYLVEVERHILTRP---NGN---GHSADVAKVHLDLSTGNPHSDAKKSSPS 420
QY 394 -----GVHCVTP-----DSGV---VGRMACSPTDHEHLLHGGQPPEGDP---- 431
Db 421 PKRTSASINGMTGLPTTQMGALDSINKYCTKVTPLNGSATINHKSSQPIINNN 480
QY 432 -----DLAKILEEVRVYIANFRFCODESAVCSWKFAACVDRCLCLMAF 475
Db 481 NIYKCANNOQKTOFEDRHPHILNELRVISARVKEEMHALQADWNFASRVVDRVCFLAF 540
QY 476 SVFTTICTIGILMSAPN 492

Db 541 SAEFLMCTAIIISYNAPH 557

RESULT 9
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25671
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: EMBL:U88167; PIDN: AAB42223.1; GSPDB: GN00019; CESP: D2092.3
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP: D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor

Query Match 37.0%; Score 999; DB 2; Length 461;
Best Local Similarity 39.8%; Pred. No. 3.2e-78;
Matches 197; Conservative 96; Mismatches 146; Indels 56; Gaps 8;

QY 12 LAASLLHVSIL-QGEF-ORUKLYKEIVKNYNPLERPVANDSOPLTIVFSLSLQIMDVDEKN 69
Db 10 LSLVLIHSNLCDCGSAETKLTLLKGNPLERPVQNSQPLEVKIKLFLQQLILDVDEKN 69
QY 70 QVLTNTLWQMSWDHVLQNVSEYPGVKTRFEP--DGQIWKPDILLYNSADERFATEH 127
Db 70 QIVSVNWLSTVTFDHLQWEPKKYIGIQIDIRFPSSDHIWKPDVLLYNSAEDFSTFK 129
QY 128 TNVLVNSSGHCQYLPFGIFKSCYIDVRWPPDVQCHCKLFGSWSYGGNSLDQM----- 182
Db 130 SNLLTYHTGTVMVPPGVLKFCQLDVTWFPDDQVCEMKFGSWTFHGAYIDLQIDDTN 189
QY 183 --QEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYPDVFTVMRRRTLYYGLMLIP 240
Db 190 GTQSMDSLTVLVNGEWOVISTNAKRVSYKCCPEPYTVNYIHRRTLYYGFNLLIP 249
QY 241 CVLISALALVLLPADSGEKISIGITVLLSLTVMLLVAEIMPATSDSVPLIAQYFAS 300
Db 250 SLLLSLMAILGFMPPDRGEKITLLEVLILAIIVFLSNVSEMTPTSEAVPLIGVFFSCC 309
QY 301 MIIVGLSVVVTIVLYQVHHDDPGGKMPKWKTRVILLNWCAMFLMRKPGEDKVRPACQHK 360
Db 310 MLVVSASVVTIVLVNLFHRSADSHENNPVLRVRLLEFLPWLFLPMSRPGYKFKV- 363
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFGLDGVHCV-TPDSGVVCGRMACSPTHDEH 419
Db 364 -----ANV-----IDSTDMKPKKPKPKPLDCLNPSNHAGYEAQ 395
QY 420 LLHGGQPPEGDPDLAKITILEEVRVYIANFRFCODESAVCSWKFAACVDRCLCLMAFSVFT 479
Db 396 ILL-----LHVSHTELRRVAVFYNKEHDERIQTDRFAAMVVDRACLLLFTVFI 445
QY 480 IICTIGILMSAPNFV 494
Db 446 VISILAINMSAPHII 460

RESULT 10
S12359
nicotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
C:Species: Schistocerca gregaria (desert locust)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: S12359

R:Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.;
EMBO J. 9, 4391-4398, 1990
A:Title: Sequence and functional expression of a single alpha subunit of an insect nicotinic
A:Reference number: S12359; MUID:91092263; PMID:1702381
A:Accession: S12359
A:Molecule type: mRNA
A:Residues: 1-557 <MAR>
A:Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <MAT>
F:245-266/Domain: transmembrane #status predicted <TM1>
F:274-295/Domain: transmembrane #status predicted <TM2>
F:308-329/Domain: transmembrane #status predicted <TM3>
F:501-523/Domain: transmembrane #status predicted <TM4>
F:47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.1%; Score 949; DB 2; Length 557;
Best Local Similarity 37.1%; Pred. No. 8.5e-74;
Matches 201; Conservative 93; Mismatches 176; Indels 72; Gaps 6;

QY 5 PGQWVLAASLLHVSQGEFQKLYKELVKNYPLRPVANDSQPLTVFSLSLQIMD 64
DB 6 PMLLLLLLLHHPAAAPDPAKLYDLSNRLIRVSNNTDTVLKGLGLSLQID 65
QY 65 VDEKNQVLTNIWLSQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLVNSADREFDA 124
DB 66 LNLKQDILLTNVLEHWDHKEPDPAPYGGYELVYSEHILWLPDILVYNNADGEYVV 125
QY 125 THTNVLNVSCHGCHQYLPFGIFKSSCYIDVRWPPFVQVCKLFGSWSGSLDQ--- 181
DB 126 TMTKAVLHHTGKVVWTPPAIFKSSCEIDVRYFPFQDQCFMKFGSWTYDGDQIDLKHN 185
QY 182 -----MQEADISGYPNGEWDLVGIPGKSERFEYCEKPEYDPVTVTMRRTLY 233
DB 186 QYDDNKVKVIGIDIREYPSVEWDILGVPAERHEKYPCCAEYPDIFNITLRRKTFY 245
QY 234 GLNLLPCVLISALALLVLLPADSGEKISLGTIVLLSLTVFLLVAEIMPATSDSVPLI 293
DB 246 TVNLIIVPCVIGISLVLVFLPADSGEKIALCISILLSTQTMFFLLSEIIPSTSLAPLL 305
QY 294 AQVFASTMIIVGSLVVTIVLYQYHHDDPGGKPKWTRVILLNWCWFLMRKRPGE--- 350
DB 306 GKYLFTWLVGLSVITIMLVNHYRKPSTHMAFWKVFTRRLPKLLMRVPEQLLA 365
QY 351 DKVRPACQKQRCRCSLAVMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRM 410
DB 366 DLAKRLLRHAHNSKLSAAAAAASSS-----AASSPDS--LRHHH 408
QY 411 ACSPTHDEHL-LHGGOPPEG----- 429
DB 409 LHQHQHHLQLHHLQRPFGCNGLHSGATNRFSGSAGAFGLPSVVGDLGSLSDVATRKYY 468
QY 430 DPDLAKILEVRVIANFRQDSEAVCSWKAACVDRCLMARSVFTIITIGILMS 489
DB 469 PFELEKAHNVLFQNHQMDQDFDADQDQWGFVAMVLDRLFLMFTIASIVGTFAIICE 528
QY 490 AP 491
DB 529 AP 530

RESULT 11
A40110
nicotinic acetylcholine receptor alpha-2 chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 20-Aug-1999
C:Accession: A40110
R:Wada, K.; Ballivet, M.; Boulter, J.; Connolly, J.; Wada, E.; Deneris, E.S.; Swanson, L.
Science 240, 330-334, 1988
A:Title: Functional expression of a new pharmacological subtype of brain nicotinic acetylcholine receptor
A:Reference number: A40110; MUID:88178113; PMID:2832952

A:Accession: A40110
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-511 <WAD>
A:Cross-references: GB:M20297; NID:g202672; PIDN:AAA40664.1; PID:g202674
A:Note: the authors translated the codon TCG for residue 494 as Cys
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match 35.0%; Score 946.5; DB 2; Length 511;
Best Local Similarity 39.1%; Pred. No. 1.3e-73;
Matches 202; Conservative 83; Mismatches 178; Indels 53; Gaps 9;

QY 8 VW-LALAASLLHVSQGEFQKLYKELVKNYPLRPVANDSQPLTVFSLSLQIMDV 65
DB 16 IMCLLIVPAVLTVQSSHTAEDRLFKHLFGGYNRWARVPVNTSDVVVRFGLSIAQLIDV 75
QY 66 DEKNQVLTNIWLSQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLVNSADREFDA 125
DB 76 DEKNQVMTTNVWLKQEWNDYKLRWDPAEFGNVTSLRVSEMIWIPDILVYNNADGEFAVT 135
QY 126 FHTNVLNVSCHGCHQYLPFGIFKSSCYIDVRWPPFVQVCKLFGSWSGSLDQMQE- 184
DB 136 HMTKAHLFTGTVHWVPPAIYKSSCSIDVTFPFQDQCKMKFGSWTYDKAKIDLEQMER 195
QY 185 -ADISGYPNGEWDLVGIPGKSERFEYCEKPEYDPVTVTMRRTLYYGLNLLTPCYL 243
DB 196 TVDLKDYWESGEWAIINATGTYNSKKYDCAIYDPVTVYFVIRRLPLFTYTNLIIPCLL 255
QY 244 ISALLVLLPADSGEKISLGTIVLLSLTVFLLVAEIMPATSDSVPLIAQVFASTMI 303
DB 256 ISCLTVLVFLPSECEKITLCISVLLSLTVFLLITEIPSTSLVPIGLSYLLFTMTF 315
QY 304 VGLSVVTVIVLYQYHHDDPGGKPKWTRVILLNWCWFLMRKRP-----GEDKVRA 356
DB 316 VTLISVITVFLVNVHRSSTHNMNWRVALLGRVPRWMMNRPLPMLHSGSPDLKLS 375
QY 357 COHKQRCRCSLAVMSAVAPPASNGNLLYIGRGLDGVHCVPTPDS--GVVCGRMACSP 414
DB 376 PSYHLEITNMDAGERETEETEEEDENICV-----CAGLPDSSMGVLVG----- 420
QY 415 THDEHLLHGG-----QPPG-----DPDLAKILEEVRYIANRFRQDSEAVCS 458
DB 421 -----HGGLHRLAMEPETKTPSOASEILLSPQIKALEGVHYIADRLSRSDADSVKE 473
QY 459 ENKFAACVVDRLCLMAFSVFTIITIGILMSAPNFV 494
DB 474 DKWYAMVVDRLFLMFLIIVSFLGTLGLFL--PPFL 507

RESULT 12
T19862
hypothetical protein C40C9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19862
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19862
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-542 <WIL>
A:Cross-references: EMBL:270266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.2
A:Map position: X
A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1;
C:Superfamily: acetylcholine receptor

Query Match 35.0%; Score 945; DB 2; Length 542;
Best Local Similarity 37.7%; Pred. No. 1.8e-73;

```
Matches 207; Conservative 93; Mismatches 165; Indels 84; Gaps 15;
QY 11 ALAASLLHV-----SLQGFQRLKYLKELVKNVNPRLRPVANDSOPLTVYFSLSLQIMDV 65
Db 12 ALHCVLHLLTEVHSSADEY--RLADLRHNDPYRPPVANASEPLWVSKYILQOILDV 69
QY 66 DEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRFPD--GOIKWPKDILLVNSADERED 123
Db 70 DEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRFPD--GOIKWPKDILLVNSADERED 129
QY 124 ATFTHTNLVNSGHCQOYLPGPIFKSSCYIDVRWFPDVQVCKLKFGSWYSGWLSLQDM- 182
Db 130 STYVNVVSVYTGDLVQVPPGILKLSCKIDITVFPDDQILCHLKFGSWYSGNFIDLRN 189
QY 183 -----QADISGIYPNGEWDLVGIPKRSERYECKEYKPYDVTVTVMRRTLYX 233
Db 190 GPEGKNIISDEGIDVQVYVQNGEWNLLAVPARHETNIFD--EQYPSLFFLYLIORTLYY 247
QY 234 GLNLLIPCVLISALALLVLLPADSGEKLISLGTIVLLSLTVFMLLVAEIMPATSDSVPLI 293
Db 248 GLNLLIPSVLISLMTVLGFTLPDAGEKITLITILLSVCFILSMVADMTPTTSEAVPLI 307
QY 294 -----AOYFASMTIIVGLSVVTVIVLYQVHHHDPDGKMPKWTIRVILLNWCWAFIRMKR 347
Db 308 GLIIFSGAFPSCCMLVVSASVFTVLVNLNHRKRPETHMSPFLREILLITWLPWLLIMRR 367
QY 348 PGEDKVRPACQKORCRCLASVEMSAVAPPASNGNLLIYG-PRGLDGVHCVPTPDG-- 404
Db 368 PG--KTIFNCTHLKAEAKKAGGSI-----KNG-----VGPKPTDSVH-----PSGLS 412
QY 405 -----VWCGR--MACSPTHDEHLHGG-----OPPEGDP----- 431
Db 413 LMKNIKLGROQITDFEFVHFVQHNLMPVAPSEMTPRVTSYKMAESYVEDVWMTLNKY 472
QY 432 -----DLAKILBEVRYANFRQDSEAVCEWKFACVVDRLCLMAFVTTIICIG 485
Db 473 MQKACLELKNISSTQAMRKMEDEDEQAANDKFAAMVVDRCCLITFSVFIWSTCG 532
QY 486 ILMSAPNFV 494
Db 533 IMPSSPHLI 541

RESULT 13
SI14703
nicotinic acetylcholine receptor beta-2 chain - goldfish (fragment)
C;Species: Carassius auratus (goldfish)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
C;Accession: SI14703
R;Hieber, V.; Bouchey, J.; Agranoff, B.W.; Goldman, D.
Nucleic Acids Res. 18, 5307, 1990
A;Title: Nucleotide and deduced amino acid sequence of the goldfish neural nicotinic ace
A;Reference number: SI14703; MUID:90384858; PMID:2402468
A;Accession: SI14703
A;Molecule type: mRNA
A;Residues: 1-459 <HTE>
A;Cross-references: EMBL:X54052; NID:G62576; PIDN:CAA37986.1; PID:g8333601
C;Superfamily: acetylcholine receptor
C;Keywords: Glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;

Query Match 34.9%; Score 942.5; DB 2; Length 459;
Best Local Similarity 38.7%; Pred. No. 2.4e-73;
Matches 190; Conservative 95; Mismatches 141; Indels 65; Gaps 8;
QY 35 KNYNPLRPVANDSOPLTVYFSLSLQIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEY 94
Db 10 ERYNKLIRPAVNVKSSQVTTIGIKVSLAQSLISVNEREQIMTNNVLTQETWTDYLVWDPNEY 69
QY 95 PGVKTVRPDGQIKWPKDILLVNSADEREDATFTHTNLVNSGHCQOYLPGPIFKSSCYIDV 154
Db 70 EGIKKLIRIPQIHMLPDLIVLNNADGVTEVSFYCNVAVNSGTGDIIFWLPALYKSALEV 129
QY 155 RWFPPDVQVCKLKFGSWYSGWLSLQDMQE--ADISGIYPNGEWDLVGIPGKRSEFYEC 212
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Db 130 RNFPPDQNCVTLKFRSWTYDRTELDTLVTSDPASRDDYTPSGEWDIVSLPGKNE----- 184
QY 213 CKEP-----YPOVTVFVWRRRTLYYGLNLLIPCVLISALALLVLLPADSGEKISLIGITV 268
Db 185 --DPNDLTLDITYDFVIRKRPFLFTINLIIIPCVLITSLAILVFLPSDCGKVTLCMSV 242
QY 269 LLSLVTFMLLVAEIMPATSDSVFLIAQYFASMTIIVGLSVVTVIVLYQVHHHDPDGKMP 328
Db 243 LLALIVFLLISKIIVPTSLAVPLIGLYKLMFTWLVTSIVTSVCLNVHHRSPSTHYMP 302
QY 329 KWTIRVILLNWCWAFIRMKRPAGEDKVRPACQKORCRCLASVEMSAVAPPASNGNLLIYG 368
Db 303 EWWKCVFLHKLPAFLIMRRPGRSNVRERFRKRGKRSFSSHQ----- 344
QY 389 FRGLDGVHCVPTPDGSGVCGMACSPTHDEHLHGGQPPEG-----DPDLAKIL 437
Db 345 -----DGSFFLTDTPGRCVCAWV-----GDLPEGSEFRQVRKVRHDDQVDEAL 369
QY 438 EEVRYIANFRQDSEAVCEWKFACVVDRLCLMAFVTTIICIGILMSAPNF----- 493
Db 390 DGVRFIAEHMKIETDDDEGIIDWKYVAMVIDRLFLWIFILVCVVGTLGLFVQ-PLFQSYN 448
QY 494 -----VEAVSKDF 501
Db 449 TPVAEEVYGD 459

RESULT 14
ACCH2N
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C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: S00377
R;Nef, P.; Oneyser, C.; Alliod, C.; Couturier, S.; Ballivet, M.
EMBO J. 7, 595-601, 1988
A;Title: Genes expressed in the brain define three distinct neuronal nicotinic acetylch
A;Reference number: S00376; MUID:88283624; PMID:3267226
A;Accession: S00377
A;Molecule type: DNA
A;Residues: 1-528 <NEF>
A;Cross-references: EMBL:X07339; NID:g62792; PIDN:CAB59645.1; PID:g6136914
C;Genetics:
A;Introns: 21/1; 73/3; 88/3; 125/2; 487/3
C;Superfamily: acetylcholine receptor
C;Keywords: Glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membran
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-528/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <NA
F;241-264/Domain: transmembrane #status predicted <TM1>
F;272-290/Domain: transmembrane #status predicted <TM2>
F;306-327/Domain: transmembrane #status predicted <TM3>
F;502-520/Domain: transmembrane #status predicted <TM4>
F;54,104/Binding site: carboxylate (Asn) (covalent) #status predicted
F;158-172,222-223/Disulfide bonds: #status predicted

Query Match 34.8%; Score 941.5; DB 1; Length 528;
Best Local Similarity 38.0%; Pred. No. 3.5e-73;
Matches 201; Conservative 85; Mismatches 174; Indels 69; Gaps 10;
QY 8 WLAL-----AASLLHVSILQGEFQRLKYLKELVKNVNLPRPVANDSOPLTVYFSLSLQIMD 64
Db 13 VWCFTVLTQATREOKQPHGFAEDRLFKHLFTGYNWRSPVPNTSDVIVKFGSLIAQLID 72
QY 65 VDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDGOIKWPKDILLVNSADEREDA 124
Db 73 VDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDGOIKWPKDILLVNSADEREDA 132
QY 125 THTNVLVNSGHCQOYLPGPIFKSSCYIDVRWFPDVQVCKLKFGSWYSGWLSLQDMQE 184
Db 133 THMTKAHLFSGKGVKVPVPAIYKSSCSIDVTFYFPDQCNCKMFGSWTYDKAKIDLENWE 192
QY 185 --ADISGIYPNGEWDLVGIPGKRSEFYECKEYKPYDVTVTVMRRTLYYGLNLLIPCV 242
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Db 193 HHVDLKDYESEGAIIINAIGRYNSKKYDCCTEIPDITTFYFVIRRLFLFYTNLIIPCL 252
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 Db 253 LISCLTVLVFLPSDCGKVTLCISVLLSLTVFLLVITETIPSTSLVPLIGEVYLL 307
 QY 303 IVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKR-----PGEDKV---- 353
 Db 313 FVTLIIITVFNHHRSPSTHTPHVRSFLLGIFRWLEPMKRPPLLLPAEGTTGQYD 372
 QY 354 RPACQKQRCRLAS-----VMSAVAPPPASNGNLLYIGRGLDG 394
 Db 373 PGTSLSTSCRLVDDVDKWEEREEEBEEREEKAYPSRPSG-----GSQG 424
 QY 395 VHCVTPTDGGVCGMACSPFTDEHLHGGQPE-----GD-----PDLAKILEE 439
 Db 425 TQC-----HYSCERQAGKAS-----GGPAPQVPLKGEYVGSQGLTSLPSILRALEG 471
 QY 440 VRYIANRPRCODESAVCSEWKFACVDRCLCLMAFSVFIICTIGILM 488
 Db 472 VQYIADHLRAEDAFSVKEDWKYVAMVIDRIFLWFIIVCLLGTGVLFL 520

RESULT 15

A53956
 nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human
 C:Species: Homo sapiens (man)
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
 C:Accession: A53956; S21338
 R:Milohovic, M.; Roses, A.D.
 Exp. Neurol. 111, 175-180, 1991
 A:Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuronal
 A:Reference number: A53956, MUID:91114756; PMID:1989896
 A:Accession: A53956
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-503 <MIH>
 A:Cross-references: GB:M37981; NID:g189252; PIDN:AAA59942.1; PID:g189253
 R:Anand, R.; Lindstrom, J.
 submitted to the EMBL Data Library, June 1990
 A:Description: Nucleotide sequence of the mature human nicotinic acetylcholine receptor
 A:Reference number: S21338
 A:Accession: S21338
 A:Molecule type: mRNA
 A:Residues: 30-503 <ANA>
 A:Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
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 A:Gene: GDB:CHRNA3
 A:Cross-references: GDB:125219; OMIM:118503
 A:Map position: 15q24-15q24
 C:Superfamily: acetylcholine receptor
 C:Keywords: neurotransmitter receptor

Query Match 34.8%; Score 940.5; DB 2; Length 503;
 Best Local Similarity 37.6%; Pred. No. 4e-73;
 Matches 192; Conservative 95; Mismatches 166; Indels 57; Gaps 8;

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 Db 8 APGAVAPRLLLLSLLFPARASAEHRLFERLFEDYNEIIRPVANVSDPVIHFVMS 67
 QY 61 QIMDVDEKNQVLTNIWLOMSWTDFYLOMNVSEYEGVKTVRFPDGOIWKPDILYNSADE 120
 Db 68 QLVKQVDEVNQIMETNLWKQIWNQYKLNWNSDYGGAEFMEVPAQKIWKPDIVLYNNAV 127
 QY 121 RFDATFHTNVLNVSCHQYLPQGIKSSCYIDVRWFFDVQHCKLKFSGWSYGGWSLDL 180
 Db 128 DFQVDDKTKALKYTGVTWIPPAIFKSSCKIDVTYFPFDYQNCYTMKFGWSYDKAKIDL 187
 QY 181 QM--QEADISGIYENGWDLVGIQKRSERYECCKEYPDYFTVTMRRRTLYVGLNLL 238
 Db 188 VLGSSMNLKDYWESGEWAIKAPGYKHDIKYNCCETIYDPDITYSLYIRRLPLFYTNLI 247

QY 239 IPCVLISALALVFLPADSGEKISGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFA 298
 Db 248 IPCLLIISFLTVLVFLPSDCGKVTLCISVLLSLTVFLLVITETIPSTSLVPLIGEVYLL 307
 QY 299 STMIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEDKVRPACQ 358
 Db 308 FTMIFVTLSIVITVFLNVHRYRPTTHTMPSWVKTVFLNLLPRVMEWTRP----- 357
 QY 359 HKQRCRLASVMSAVAPPPASNGNLLYIGRGLDGVHCVTPTDPS-----GVVCGMACS 413
 Db 358 -----TSNEGNAQRPRLYGAE-----LSNLCFSRAESKGCKEGYPCQDGMCG 401
 QY 414 PTHDEHL-----LHGGQPEG-----DPLAKILEEVRYIANRPRCODESEA 455
 Db 402 YCHHRIKISFNFSANLTRSSSESVDVLSLSALSPEIKETKAIQSVKYIAENKKAQNEAKE 461
 QY 456 VCSEWKFACVDRCLCLMAFSVFIICTIG 485
 Db 462 IQDDWKYVAMVIDRIFLW---VFTLVCLIG 488

Search completed: May 5, 2004, 15:32:01
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:31:33 ; Search time 49 Seconds
(without alignments)
2839.779 Million cell updates/sec

Title: US-09-703-951A-12

Perfect score: 2702

Sequence: 1 MRCSGGVWLAALAAALHVS.....TIGILMSAFNEVAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2702	100.0	502	9	US-09-892-985-8
2	2698	99.9	502	10	US-09-954-936-2
3	2697	99.8	502	15	US-10-434-364-4
4	2694	99.7	502	15	US-10-352-684A-56
5	2674	99.0	502	15	US-10-434-364-27
6	2546	94.2	502	15	US-10-434-364-10
7	2026	75.0	446	14	US-10-349-836-12
8	1258.5	46.6	501	9	US-09-303-232-6
9	1246	46.1	496	9	US-09-303-232-4
10	1159.5	42.9	770	9	US-09-303-232-2
11	1108.5	41.0	498	15	US-10-369-493-6415
12	1093.5	40.5	560	15	US-10-369-493-5169
13	1092	40.4	554	14	US-10-203-968-12
14	999	37.0	461	15	US-10-369-493-5084
15	963	35.6	622	9	US-09-941-179A-11

16	949	35.1	529	14	US-10-349-836-2	Sequence 2, Appli
17	947	35.0	622	9	US-09-941-179A-3	Sequence 3, Appli
18	945	35.0	542	15	US-10-369-493-6980	Sequence 6980, Ap
19	937	34.7	502	14	US-10-157-031-92	Sequence 92, Appl
20	936	34.6	504	14	US-10-349-836-4	Sequence 4, Appli
21	932.5	34.5	631	9	US-09-941-179A-7	Sequence 7, Appli
22	924.5	34.2	528	9	US-09-892-985-2	Sequence 2, Appli
23	920	34.0	627	14	US-10-349-836-6	Sequence 6, Appli
24	912	33.8	504	9	US-09-892-985-4	Sequence 4, Appli
25	885	32.8	498	14	US-10-349-836-18	Sequence 18, Appl
26	875.5	32.4	450	9	US-09-795-693-11	Sequence 11, Appl
27	875.5	32.4	450	14	US-10-156-239-11	Sequence 11, Appl
28	875.5	32.4	450	14	US-10-199-485-11	Sequence 11, Appl
29	871.5	32.3	450	15	US-10-312-088-38	Sequence 38, Appl
30	871.5	32.3	494	14	US-10-349-836-10	Sequence 10, Appl
31	871.5	32.3	494	15	US-10-303-198-2	Sequence 2, Appli
32	870	32.2	498	9	US-09-892-985-12	Sequence 12, Appl
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34	867.5	32.1	529	9	US-09-795-693-31	Sequence 31, Appl
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36	867.5	32.1	529	14	US-10-199-485-31	Sequence 31, Appl
37	865	32.0	502	9	US-09-892-985-10	Sequence 10, Appl
38	865	32.0	502	14	US-10-349-836-14	Sequence 14, Appl
39	846	31.3	457	14	US-10-157-031-28	Sequence 28, Appl
40	842	31.2	437	14	US-10-261-798-69	Sequence 69, Appl
41	838.5	31.0	468	15	US-10-369-493-5462	Sequence 5462, Ap
42	832	30.8	534	15	US-10-369-493-5029	Sequence 5029, Ap
43	803	29.7	449	14	US-10-199-995-2	Sequence 2, Appli
44	803	29.7	479	14	US-10-349-836-20	Sequence 20, Appl
45	799.5	29.6	479	14	US-10-203-968-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779

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; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8

Query Match 100.0%; Score 2702; DB 9; Length 502;
Best Local Similarity 100.0%; Pred. No. 4.4e-263;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 QIMVDKXNQVLTINILQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLNSADE 120
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DB 121 RFDATFHTNVLNVSCHCOYLPPIGIFKSSCYIDVRWFFPDVQHCCKLKFSGWSYGGW 180
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DB 181 QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEYPDPVTFTVTRRTLYYGLNLLIP 240
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DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTWVILLNWCAMFLRMKRGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKWTWVILLNWCAMFLRMKRGEDKVRPACQHK 360
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DB 361 QRCCLSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPPTDPSGVVCGRMACSPTHDEHL 420
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DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2
US-09-954-936-2
; Sequence 2, Application US/09954936
; Publication No. US20030073161A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
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; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-09-954-936-2

Query Match 99.9%; Score 2698; DB 10; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.1e-262;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 QIMVDKXNQVLTINILQMSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLNSADE 120
QY 121 RFDATFHTNVLNVSCHCOYLPPIGIFKSSCYIDVRWFFPDVQHCCKLKFSGWSYGGW 180
DB 121 RFDATFHTNVLNVSCHCOYLPPIGIFKSSCYIDVRWFFPDVQHCCKLKFSGWSYGGW 180
QY 181 QMOEADISGYIPNGEWDLVGIPGKRSERFYECCKEYPDPVTFTVTRRTLYYGLNLLIP 240
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QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
US-10-434-364-4
; Sequence 4, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND QM-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; TITLE OF INVENTION: THE TRANSFECTED CELLS
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-434-364-4
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; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-352-684A-56

Query Match          99.7%; Score 2694; DB 15; Length 502;
Best Local Similarity 99.6%; Pred. No. 2.8e-262;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  MRCSPGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60
Db      1  MRCSPGVWLAALASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60

QY      61  QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120
Db      61  QIMDVDEKQVLTNTIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120

QY      121  RPDATHTNVLVNNSGHCQVLPGIFKSSCYIDVRWFPDVOHCKLKFGWSYCGWSL 180
Db      121  RPDATHTNVLVNNSGHCQVLPGIFKSSCYIDVRWFPDVOHCKLKFGWSYCGWSL 180

QY      181  QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
Db      181  QMQEADISGYIPNGEWDLVGIPKRSERFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240

QY      241  CVLISALALLVFLPADSGEKISLIGITVLISLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
Db      241  CVLISALALLVFLPADSGEKISLIGITVLISLTVFMLLVAEIMPATSDSVPLIAQYFAST 300

QY      301  MIIVGLSVVTVIVLVQVHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEDKVRPACQHK 360
Db      301  MIIVGLSVVTVIVLVQVHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEDKVRPACQHK 360

QY      361  QRRCSLASVEMSAVAPPASNGNLLITGFRGLDGVHCVPPTDSDGVVCGRMACSPTHDEHL 420
Db      361  QRRCSLASVEMSAVAPPASNGNLLITGFRGLDGVHCVPPTDSDGVVCGRMACSPTHDEHL 420

QY      421  LHGGQPEGGDPLAKILIEVRYIYIANNRFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db      421  LHGGQPEGGDPLAKILIEVRYIYIANNRFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480

QY      481  ICTIGILMSAPNFVEAVSKDFA 502
Db      481  ICTIGILMSAPNFVEAVSKDFA 502

RESULT 5
US-10-434-364-27
; Sequence 27, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DANGUANG
; TITLE OF INVENTION: QM-7 AND QT-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; TITLE OF INVENTION: THE TRANSFECTED CELLS
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1

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; SEQ ID NO 27
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-434-364-27

Query Match          99.0%; Score 2674; DB 15; Length 502;
Best Local Similarity 98.8%; Pred. No. 2.9e-260;
Matches 496; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSEGGWALAAALLHVSQGEFQRLYKELVNKNYPLRPVANDSQPLTVYFSLQIMDV 60
Db 1 MRCSEGGWALAAALLHVSQGEFQRLYKELVNKNYPLRPVANDSQPLTVYFSLQIMDV 60
QY 61 QIMQVDEKQVLTNNIWLQMSWTDHYLQNVSEYGVKTVRFPDQGIWKPDIILLNSADE 120
Db 61 QIMQVDEKQVLTNNIWLQMSWTDHYLQNVSEYGVKTVRFPDQGIWKPDIILLNSADE 120
QY 121 RFDATFHTNVLNSSGHCQYLPPIGIFKSSCYIDVRWFFDVQHCCKLFGSWSYGGWSLDL 180
Db 121 RFDATFHTNVLNSSGHCQYLPPIGIFKSSCYIDVRWFFDVQHCCKLFGSWSYGGWSLDL 180
QY 181 QMQEADISGYPNGEWDLVIGIPKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYPNGEWDLVIGIPKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGTITVLSLTVFMLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGTITVLSLTVFMLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQHHDHDPGGMKPKWTRVILLNCAWFLMRKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLYQHHDHDPGGMKPKWTRVILLNCAWFLMRKPGEDKVRPACQHK 360
QY 361 QRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPDSGVVCGMACSPHDEHL 420
Db 361 QRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPDSGVVCGMACSPHDEHL 420
QY 421 LHGGQPPGDDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFEAVSKDFA 502
Db 481 ICTIGILMSAPNFEAVSKDFA 502

RESULT 6
US-10-434-364-10
; Sequence 10, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND QT-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-434-364-10

Query Match          94.2%; Score 2546; DB 15; Length 502;
Best Local Similarity 93.8%; Pred. No. 2.3e-247;
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGVWLAAASLLHVSQGEFQRLYKELVNKNYPLRPVANDSQPLTVYFSLQIMDV 65
Db 6 GGVWLAAASLLHVSQGEFQRLYKELVNKNYPLRPVANDSQPLTVYFSLQIMDV 65
QY 66 DEKQVLTNNIWLQMSWTDHYLQNVSEYGVKTVRFPDQGIWKPDIILLNSADERFAT 125
Db 66 DEKQVLTNNIWLQMSWTDHYLQNVSEYGVKTVRFPDQGIWKPDIILLNSADERFAT 125
QY 126 PHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFFDVQHCCKLFGSWSYGGWSLDLQMQEA 185
Db 126 PHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWFFDVQHCCKLFGSWSYGGWSLDLQMQEA 185
QY 186 DISGIYPNGEWDLVIGIPKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIPCVLIS 245
Db 186 DISGIYPNGEWDLVIGIPKRSERFYECKEYPDVTFTVMRRRTLYYGLNLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLGTITVLSLTVFMLVAEIMPATSDSVPLIAQYFASTMIIVG 305
Db 246 ALALLVFLPADSGEKISLGTITVLSLTVFMLVAEIMPATSDSVPLIAQYFASTMIIVG 305
QY 306 LSVVTVTVLYQHHDHDPGGMKPKWTRVILLNCAWFLMRKPGEDKVRPACQHKQRRC 365
Db 306 LSVVTVTVLYQHHDHDPGGMKPKWTRVILLNCAWFLMRKPGEDKVRPACQHKQRRC 365
QY 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPDSGVVCGMACSPHDEHLHGGQ 425
Db 366 LASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPDSGVVCGMACSPHDEHLHGGQ 425
QY 426 PPEGDDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTICTIG 485
Db 426 PPEGDDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTICTIG 485
QY 486 ILMGAPNFEAVSKDFA 502
Db 486 ILMGAPNFEAVSKDFA 502

RESULT 7
US-10-349-836-12
; Sequence 12, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
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; SEQ ID NO 6
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-303-232-6

Query Match 46.1%; Score 1258.5; DB 9; Length 501;
Best Local Similarity 48.6%; Pred. No. 1.5e-117;
Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;

QY 10 LALAASLLHVSLOGEQRKLYKELVKNYNPLRPVANDSQPLTYVYFSLSLQIMDVDEKN 69
Db 8 LALLA-LLPVSEQGPHEKRLNALLANYNTLERPVANESPLEVRGLTQQIDVDEN 66
QY 70 QVLTNNIWLQMSWDHYLQWNVSEYGVKTVRPDQGLWKPDPDILLVNSADERFDATEHTN 129
Db 67 QLSITNWLISLEWNYLNRWNSSEYGVKDLRTPNKLWKPDLVLYNSADEGFGTGTQTN 126
QY 130 VLYNSGHCOYLLPPGIFKSCSYIDVRFPFDVQHKCLKFGWSYGGWSLDLQWQ---AD 186
Db 127 VVVRSGSCLYVPPGIFKSTCKMDIAWFDPDDQHKCDMKFGSWTYDGNQLDLVLKDEAGD 186
QY 187 ISGYIPNGEWDLVGIQKRSERYEYCKEYPPDVFTVWRRRTLYXGLNLLIPCVLISA 246
Db 187 LSDFITNGEYWLGMGPKNNTIYACPEYVDVFTTIMITRRRLTYFFNLVIVPCVLISS 246
QY 247 LALLVFLPADSGEKISLGIITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASPMIIVGL 306
Db 247 MALLGFTLPDPSGEKLTGVTILLSTLVFLNVAETLPQVSDALPLLGTGYFCIMFVVAS 306
QY 307 SVVTVTVLVQYHHHPDGGKMPKWTVRVILLNWCANFLMRKPGEDKVPACQHKQRCSL 366
Db 307 SVVLTVVVLNYHRTADIHMPQWIKSVFLQWLFWILMRSPGKKITRKTIMMTRMREL 366
QY 367 ASVEMSAVA-----PPP-----ASGNLLYIGFRLGDGVHCVPDPDSGVVC 407
Db 367 ELKERSKSLANVLIDDDFRHGPPPPNSTASTGNL-----GGPC 407
QY 408 G-----RMACSPTDEHLLHGQPDGPDPLAKILLEVRYIANRFRCODESEAVCSEW 460
Db 408 SIFRTDPRRSFVRPSTMEDV--GGGLGSHRELHLILRELQFIARMKKADEAEELISDW 465
QY 461 KEAACVVDRLCLMAFSVFTIICITIGILMSAPNFV 494
Db 466 KFAAMVVDRECLFVFTFLTIATVAVLSAPHHI 499

RESULT 9
US-09-303-232-4
; Sequence 4, Application US/09303232A
; Patent No. US2002000657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; TITLE OF INVENTION: Insect acetylcholine receptor subunits
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: DE 198 19 829.9
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-303-232-4

Query Match 46.1%; Score 1246; DB 9; Length 496;
Best Local Similarity 46.0%; Pred. No. 2.6e-116;
Matches 240; Conservative 86; Mismatches 126; Indels 70; Gaps 6

QY 4 SPGGVYLAARASLLHVS-QGSEQRKLYKELVKNYNPLRPVANDSQPLTYVYFSLSLQIM 63

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Db 12 APAGLLLLCLLWPRGARGVGEKRLHLLHLDHYNVLERPVVNSDPLQLSGLTLMQII 71
QY 64 DVDEKXQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPDPQIQWKPDIILVNSADERD 123
Db 72 DVDEKXQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPDPQIQWKPDIILVNSADERD 131
QY 124 ATFTNVLNNSGHCQYLPFGKSSCYIDVRWFPDQVHCKLKFSGWSYGGWSLDLQMQ 183
Db 132 STYPTNVVRNNGSCLYVPPGFKSTCKIDITWFPDDQRCCKMFGSWYDGVQLDLQ 191
QY 184 E---ADISYIPNGEWDLVGIPCKRSERFYECCKEYPDVTVTVMRRRTLYYGLNLLIP 240
Db 192 DEGGDISFVNGEWELIGVPGKREIYVNCCEPYDITFAVWIRKRTLYFFNLIVP 251
QY 241 CVLISALALLVLLPADSGEKISLGLTLLSVFVLLVAEIMPATSDSVPLIAQYFAST 300
Db 252 CVLIASALLGFTLPPDSEKLSLGLTLLSVFVLLVAEIMPATSDSVPLIAQYFAST 311
QY 301 MIIVGLSVVTVIQLYHHDDPGGKMPKRWTRVILLNWCANFLMRKRPGEDEKVRPACQHK 360
Db 312 MFVASSVSTIILINYYHRAHTEMSDWIRCVELYWLPWLRMSRPG----- 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPDPDGSVVGCRMACSPH----- 416
Db 361 -----SATTPPPAR-----VPPPPDLERRSKSLLANVLD 392
QY 417 -DEHLLH-----GGQPPG-----DPLAKILBEVRYIANRFRQDE 452
Db 393 IDDFRHPQAOQQCCRYGGEENGAGLAHSCFGVDYLSLILKEIRVITQMRKDE 452
QY 453 SEAVCSWKEFAACVDRCLMAFVSFTIICITIGILMSAPNFV 494
Db 453 DADISRDWKFAAMVVDRLCLLIIFTLFIATLAVLLSAPHIM 494

RESULT 10

US-09-303-232-2
; Sequence 2, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; TITLE OF INVENTION: Insect acetylcholine receptor subunits
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: DE 198 19 829.9
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-303-232-2

Query Match 42.9%; Score 1159.5; DB 9; Length 770;
Best Local Similarity 45.1%; Pred. No. 2.7e-107;
Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

QY 8 VWLAAALLHVSLOGEFQ-RKLYKELVKNYNPLERPVANDSQPLTVYFSLQLQIMVD 67
Db 297 IYVNLKSAK---VCLAGYHEKRLHLLDLPYNTLERPVLESPLQLSGLTLMQIIDVDE 353
QY 68 KNOVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPDPQIQWKPDIILVNSADERD 127
Db 354 KNOVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPDPQIQWKPDIILVNSADERD 413
QY 128 TNLVNSSGHCQYLPFGKSSCYIDVRWFPDQVHCKLKFSGWSYGGWSLDLQMQE--- 184
Db 414 TNLVNSSGHCQYLPFGKSSCYIDVRWFPDQVHCKLKFSGWSYGGWSLDLQMQE--- 473

QY 185 ADISYIPNGEWDLVGIPCKRSERFYECCKEYPDVTVTVMRRRTLYYGLNLLIPCVLI 244
Db 474 GDISSYVLNGEWELIGVPGKREIYVNCCEPYDITFAVWIRKRTLYFFNLIPCVLI 533
QY 245 SALALLVLLPADSGEKISLGLTLLSVFVLLVAEIMPATSDSVPLIAQYFASTMIIV 304
Db 534 ASMALLGFTLPPDSEKLSLGLTLLSVFVLLVAEIMPATSDSVPLIAQYFASTMIIV 581
QY 305 GLSVVVTVIQLYHHDDPGGKMPKRWTRVILLNWCANFLMRKRPGEDEKVRP-ACQHKQR 363
Db 582 -----WIRVFLCMLPWLRMSRPG-----RPLILFFPTTP 612
QY 364 CSLASVE-----MSAVAPPPASNGNLLY-----IGFRLDGVHCVP-TP----- 401
Db 613 CSDDTSERKQHLSDVELKERSSKSLLANVLDIDDDFH-----NCRPMTPGTLPHPAF 668
QY 402 -----DSGVV-----CGRMACSPHDEHLLHGGQPPGDPDLAKILBEVRYIANRFR 449
Db 669 YRTVYGGDDGSGIGPIGSTRMPDAVTH-----HTCIKSTVEYELGLILKEIRFITDQLRK 723
QY 450 QDESEAVCSWKEFAACVDRCLMAFVSFTIICITIGILMSAPNFV 494
Db 724 DDECNDIANDWKFAAMVVDRLCLLIIFTLFIATLAVLLSAPHII 768

RESULT 11

US-10-369-493-6415
; Sequence 6415, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6415
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6415

Query Match 41.0%; Score 1108.5; DB 15; Length 498;
Best Local Similarity 44.6%; Pred. No. 1.9e-102;
Matches 226; Conservative 77; Mismatches 167; Indels 37; Gaps 7;

QY 10 LALAASLLHVSLOGEFQ-RKLYKELVKNYNPLERPVANDSQPLTVYFSLQLQIMVD 68
Db 6 LLISCAILAAPTLGLQERLYEDLMRYNNLRPVANHSEPVTVHLKVALQIQIIDVDEK 65
QY 69 NQVLTNNIWLQMSWTDHYLQWNVSEYGVKTVRPDPQIQWKPDIILVNSADERD 128
Db 66 NQVYVNAWLDYTNWYDCAEYGNITDVRFPAGKIWKPDVLLNSVDTFNDSYQ 125
QY 129 NTVNSSGHCQYLPFGKSSCYIDVRWFPDQVHCKLKFSGWSYGGWSLDLQMQEA--D 186
Db 126 NMIVSYTGLVHWVPPGIFKISCKIDIQWFFDEQKCFKFGSWYDGYLDLQATGQ 185
QY 187 ISGYIPNGEWDLVGIPCKRSERFYECCKEYPDVTVTVMRRRTLYYGLNLLIPCVLI 246
Db 186 ISEYISNGEWALPLTTVERNEKFYDCCPEYDPVHVHLMRRRTLYYGFNLIMPCILTL 245
QY 247 LALLVLLPADSGEKISLGLTLLSVFVLLVAEIMPATSDSVPLIAQYFASTMIIVGL 306
Db 246 MTLGLFTLPPDAGEKITLIQTIVLLSICFFLSIVSEMSPTSEAVPLLGIFFTCMIVVTA 305

QY 307 SVVTVTVILQYHHDDPGKMPKWTVRVILLNWCWFLRMKRPGEKVRPACQKQRCSL 366
DB 306 STVFTVTVLNLHRTPTTHDMGPTNRLLLYWPLRMKRP-----HNLTVASL 356
QY 367 ASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPPDS-----GVVCGRMAC 412
DB 357 PSL-----FSTKPNRHSLSLRNIK--DNEHSLSRANSFDACRLNQVIMTQSVNGLTSL 410
QY 413 SPTHDEHLLHGGQPPGDPD-----LAKILEEYVIANRFRCDSEAVCSWKFAACVV 467
DB 411 GSIPSTWISNGTTTDSVQQATLLILHRIYHELKIVTKRMIEGDKESQACNNWKAAMVV 470
QY 468 DRCLMAFSVFTIICIGILMSAPNFV 494
DB 471 DRCLXYVFTIIVSTIGIFWSAPYLV 497

RESULT 12
US-10-369-493-5169
; Sequence 5169, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5169
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5169

Query Match 40.5%; Score 1093.5; DB 15; Length 560;
Best Local Similarity 40.8%; Pred. No. 7.4e-101;
Matches 227; Conservative 93; Mismatches 156; Indels 81; Gaps 9;
QY 10 LALAASLL-----HVSILQSGFQRLKYLKVNYPLEPVPANDSOPLTVYFSLSLQI 62
DB 8 LVLSVILTWETKCSKVITWGDHERRLYAKLAENKRLARPVRNSEAVVLLGMDYQOI 67
QY 63 MDVDEKQVLTNNIWLMSWTDHLYQWNVSEYPGVKTVPDQGIWKPDILLYNSADERF 122
DB 68 LDIDEKHQIMNSVNLMSWTDHLYTWDPSFNGIKVRLPNNIWKPDVLLYNSVDQOF 127
QY 123 DATFTNNVLNNSGHCQYLPQGIKSSCYIDVRWFFDVQHCCLKFSGWSYGSWLDLQ 182
DB 128 DSTMPVNAVLYTGNVTWIPPAIRSSCAIDIAFPFDTHCTMKFGSWTSGFTDLIN 187
QY 183 QEADISGYTPNGEWDLVGIPGKRSERYECCKEPPYDVTVTMMRRRTLYGLNLLIPC 242
DB 188 TTISPATYKNGEWELLGTSQRSIFFECCPEPYDVTVTTSIRRTLYYGFNLLPCN 247
QY 243 LISALLVFLPADSGEKISIGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFASMTI 302
DB 248 LISSALLSFTLPADCGEKLNGVTIFMSLCVPMVIAEAMPQTSALPLIQIFSCIMF 307
QY 303 IVGLSVVTVTVILQYHHDDPGK--MPKTRVILLNWCWFLRMKRPGEKVRPACQH-- 359
DB 308 QVGASVATVIALNFHRSPEQYKPMNKFLLKLLGMLPTLLGMERPDVLELSVHGAHYA 367
QY 360 ----KQRCCLASVEMSAVAPPASNGNLLYIGRGLD----- 393
DB 368 SDNKKQKQRYLIEVERHILTRP---NGN-----GHSVAVDKAVHLDLSTGNPHSDAKKSSFS 420

QY 394 -----GVHCVPTP-----DSGV---VCGRMACSPTHDEHLLHGGQPPGDP----- 431
DB 421 PKRTSASIMGWGLPTQMGALDSSINKYCTKTVRPLENGSATINHKSSPOINPINN 480
QY 432 -----DLAKILEEYVIANRFRCDSEAVCSWKFAACVDRCLCMAF 475
DB 481 NIYKCANNOKTQPEDRHHFHLNRLRVISARVKEAMHALQADWMPASFVRVDRVCLAF 540
QY 476 SVFTIICIGILMSAPN 492
DB 541 SAFLFMCATLISYNAPH 557

RESULT 13
US-10-203-968-12
; Sequence 12, Application US/10203968
; Publication No. US20030186370A1
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
; APPLICANT: TROMWELL, Stephen Charles
; APPLICANT: EAST, Peter David
; APPLICANT: LIAO, Chunyan
; APPLICANT: DUMANCIC, Mira Maria
; TITLE OF INVENTION: 5HT3 Receptors of Nematodes, Polynucleotide Molecules Encoding;
; TITLE OF INVENTION: Antagonists Thereof
; FILE REFERENCE: 050179-0106
; CURRENT APPLICATION NUMBER: US/10/203,968
; CURRENT FILING DATE: 2002-08-15
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: PCT/AU01/00150
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-203-968-12

Query Match 40.4%; Score 1092; DB 14; Length 554;
Best Local Similarity 40.6%; Pred. No. 1e-100;
Matches 224; Conservative 95; Mismatches 159; Indels 74; Gaps 8;
QY 8 VVLAASLLHVSLLQSGFQRLKYLKVNYPLEPVPANDSOPLTVYFSLSLQIMDYDE 67
DB 7 IGIAFPFALFRVITWGDHERRLYAKLAENKRLARPVRNSEAVVLLGMDYQOILDIDE 66
QY 68 KNOVLTTNNIWLMSWTDHLYQWNVSEYPGVKTVPDQGIWKPDILLYNSADERFATFH 127
DB 67 KHQIMNSVNLMSWTDHLYTWDPSFNGIKVRLPNNIWKPDVLLYNSVDQDFSTWP 126
QY 128 TNNVLNNSGHCQYLPQGIKSSCYIDVRWFFDVQHCCLKFSGWSYGSWLDLQMEADI 187
DB 127 VNAVLYTGNVTWIPPAIRSSCAIDIAFPFDTHCTMKFGSWTSGFTDLINTTISP 186
QY 188 SCYIPNGEWDLVGIPGKRSERYECCKEPPYDVTVTMMRRRTLYYGLNLLIPCULISAL 247
DB 187 ATYKNGEWELLGTSQRSIFFECCPEPYDVTVTTSIRRTLYYGFNLLPCMLISSL 246
QY 248 ALLVFLPADSGEKISIGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFASMTIIVGLS 307
DB 247 ALLSFTLPADCGEKLNGVTIFMSLCVPMVIAEAMPQTSALPLIQIFSCIMFQVGAS 306
QY 308 VVVTVTVILQYHHDDPGK--MPKTRVILLNWCWFLRMKRPGEKVRPACQH-----K 360
DB 307 VVATVIALNFHRSPEQYKPMNKFLLKLLGMLPTLLGMERPDVLELSVHGAHYASDNKK 366
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGRGLD----- 393
DB 367 KQRYLIEVERHILTRP---NGN-----GHSVAVDKAVHLDLSTGNPHSDAKKSSPSPKRTS 419
QY 394 -----GVHCVPTP-----DSGV---VCGRMACSPTHDEHLLHGGQPPGDP----- 431

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Db 420 ASIMGTLPTQMGALDSSINKYCTKTRPLENGSATINKHSSQINNNNNIYKC 479
QY 432 -----DLAKILEEYRIANRFRCDSEAVCEWKFPAACVDRCLCMAPSVFTI 480
Db 480 ANNOQTQEDRHFHILNELRVISARVKEEAMHALQADWMFASRVVDVRCFLAFSAFLF 539
QY 481 ICTIGILMSAPN 492
Db 540 MCTAISYNAPH 551

RESULT 14
US-10-369-493-5084
; Sequence 5084, Application US/10369493
; Publication NO. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5084
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5084

Query Match 37.0%; Score 999; DB 15; Length 461;
Best Local Similarity 39.8%; Pred. No. 1.9e-91;
Matches 197; Conservative 96; Mismatches 146; Indels 56; Gaps 8;

QY 12 LAASLHVSL-QGEF-ORLYKELVKNYNPLRPVANDSOPLYVYSLSLQIMVDEKN 69
Db 10 LSLVITHSNLDCGSAETKLFDTLLAGYNPLRPVQNSQPLEVKIKLFQQQLDLYDEKN 69
QY 70 QVLTITNWLQMSWTDVYLVQNVSEYGVKTVRPP--DGLWKPDILLYNADRFDATEH 127
Db 70 QIVSVNAWLSYTFWFDHKLQWEPKYGIGQIRFPGSSDHLWKPDVLLYNSAAEDFSTFX 129
QY 128 TNVLVNSSGHCQYLPFGIFKSSCYIDVRFPFDVQHCKLFGWSYSGWSLDLQM----- 182
Db 130 SNLLTYHTGTVMIPGVLKFCQLDVTWFPDDQVCEMFGSWTFHGYAIDLQIDDDTN 189
QY 183 --QADISGYPNGEWDLVGIPKRSRPFYECCKEYPDVTFTVMRRRTLYGLNLIP 240
Db 190 GTQSMDSLTVNGVEQVISTNAKRVVSYKCCPEYPTVNYLHIHRRRTLYYGFNLIP 249
QY 241 CVLISALALVFLPADSGEKISLIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 250 SLLISLMAILGFMFPDAGEKITLEVILLAIIVFLSNVSEMTPTSEAVPLIGVFFS 309
QY 301 MIIVGLSVVTVIVLQVHHDDPGGKMPKTRVILLNWCAMFLRMKRPGEKVPACQHK 360
Db 310 MLVVSASVFTIVLNLHFRSADSHENNPVRRVLLFPLWLLFMSRPGYKFKV----- 363
QY 361 QRRCLASVENSAPVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEH 419
Db 364 -----ANV-----IDSTDKMPKPKPNPLDCLNPSNAGYEAQ 395
QY 420 LLHGQOPGEGDPLAKILEEVRYIANRFRCDSEAVCEWKFPAACVVDRLCLMAFSVFT 479
Db 396 ILL-----LHVSHTELRRVVAFTNKEHDERIQTDWRFAAMVVDRACLLLFTVFI 445
QY 480 ICTIGILMSAPNFV 494
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Db 446 VISILAIMSAPHII 460
RESULT 15
US-09-941-179A-11
; Sequence 11, Application US/09941179A
; Patent No. US20020146765A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Acetylcholine receptor subunits
; FILE REFERENCE: Le A 34 821
; CURRENT APPLICATION NUMBER: US/09/941,179A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: DE 100 42 177.6
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
; OTHER INFORMATION: receptor
US-09-941-179A-11

Query Match 35.6%; Score 963; DB 9; Length 622;
Best Local Similarity 34.5%; Pred. No. 1.2e-87;
Matches 210; Conservative 90; Mismatches 185; Indels 124; Gaps 9;

QY 4 SPGGVWLALASLL-----HVSLLQGEFQRLKYELVKNYNPLRPVANDSOPLYVYSLSL 59
Db 6 SKGNLALLLCASIFPAFGHVTETRAHAERLLKLFSGYNKMSRPVANISDVVLVRFGLSI 65
QY 60 LQIMDVDEKNQVLTNWLQMSWTDVYLVQNVSEYGVKTVRFPDGLWKPDILLYNSAD 119
Db 66 AQLIDVDENKQMTNVVVKQEWHDYKURDPOEYENVTSLRIPSELNWRPDVLYNNAD 125
QY 120 ERFDATEHNVLVNSSGHCQYLPFGIFKSSCYIDVRFPFDVQHCKLFGWSYSGWSLD 179
Db 126 GDFAVTHLTAKHLFDYDGRILKNWPPALYKSSCSIDVTFPFDQDQCKMKGSTYDKAKID 185
QY 180 L--QMOEADISGYPNGEWDLVGIPKRSRPFYECCKEYPDVTFTVMRRRTLYYGLNL 237
Db 186 LVSMHSHVDLSEFYTSVENDILEVPAVRNEKFTCCDEPYLDITFIRRLPLFTYINL 245
QY 238 LTPCVLISALALVFLPADSGEKISLIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYF 297
Db 246 IIPCLLISCLTVLVFLPSECGEKITLCISVLLSLVFLLLITLITPSTSLVPLIGEYL 305
QY 298 ASTMIIVGLSVVTVIVLQVHHDDPGGKMPKTRVILLNWCAMFLRMKRPGE----- 349
Db 306 LFTWIFVTLISIIITVFLVNLVHHSRPTHTMPDWRVRVFLDIVPRLLFMKRPSTVDKNCCK 365
QY 350 -----EDKVRPACQHKOR 362
Db 366 LIESMHKLTNSPRLWSETDMEPNFTTSSPSPQSNFPTSPSCAHLLEPAKPMCKSPSG 425
QY 363 RCSLASVE---MSAVAPPPA-----SNGNLL-----YIGFRGLD 393
Db 426 QYSLMHEPPEPQVTCSSPKPSCHEPLSDTQTTISLKSRLSVQOYSPNKPTEGSIKRSRS 485
QY 394 GVHCVPFPDGSVCGRMACSP-----HDEHLH-----GGQPEG----- 429
Db 486 IQCYLQEDSSQTNHSHSSASPASQRCNLNEEQPHKPHQCKCKRKGAAAGTPTQGSKSH 545
QY 430 -----DPLAKILEEVRYIANRFRCDSEAVCEWKFPAACVVDRLCLMAFSVFT 479
Db 546 SNKGEHLVMSPALKLAVEGVHYIADHLRAEDADFSVKEDWKYVAMVIDRFLMFMFIIVC 605
QY 480 ICTIGILM 488
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Db 606 LLGTVGLFL 614
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Search completed: May 5, 2004, 15:37:26
Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:28:53 ; Search time 22 Seconds
(without alignments)
1178.011 Million cell updates/sec

Title: US-09-703-951A-12
Perfect score: 2702
Sequence: 1 KRCSFGVWLAASILHVS.....TIGILMSAPFVEAVSKDFA 502

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCFUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2702	100.0	502	2	US-08-466-589-8
2	2702	100.0	502	2	US-08-700-636-8
3	2702	100.0	502	3	US-08-467-574-8
4	2702	100.0	502	4	US-09-217-345-8
5	2702	100.0	502	4	US-08-487-596-12
6	2702	100.0	502	4	US-09-892-985-8
7	2698	99.9	502	4	US-08-771-737-2
8	2698	99.9	502	4	US-09-954-936-2
9	2544	94.2	502	1	US-08-278-635B-7
10	2544	94.2	502	3	US-08-464-258B-7
11	2544	94.2	502	3	US-08-471-961-7
12	2544	94.2	502	4	US-09-345-109C-7
13	2026	75.0	446	4	US-08-660-451A-12
14	1820.5	67.4	511	1	US-08-278-635B-8
15	1820.5	67.4	511	3	US-08-464-258B-8
16	1820.5	67.4	511	3	US-08-471-961-8
17	1820.5	67.4	511	4	US-09-345-109C-8
18	949	35.1	529	1	US-08-496-855A-2
19	949	35.1	529	4	US-08-487-596-2
20	949	35.1	529	4	US-08-660-451A-2
21	947	35.0	510	1	US-08-278-635B-4
22	947	35.0	510	3	US-08-471-961-4
23	947	35.0	510	4	US-09-345-109C-4
24	944.5	35.0	511	3	US-08-464-258B-4
25	936	34.6	504	4	US-08-660-451A-4
26	924.5	34.2	528	2	US-08-466-589-2
27	924.5	34.2	528	2	US-08-700-636-2

28	924.5	34.2	528	3	US-08-467-574-2	Sequence 2, Appli
29	924.5	34.2	528	4	US-09-217-345-2	Sequence 2, Appli
30	924.5	34.2	528	4	US-09-892-985-2	Sequence 2, Appli
31	920	34.0	627	4	US-08-660-451A-6	Sequence 6, Appli
32	912	33.8	504	2	US-08-466-589-4	Sequence 4, Appli
33	912	33.8	504	2	US-08-700-636-4	Sequence 4, Appli
34	912	33.8	504	3	US-08-467-574-4	Sequence 4, Appli
35	912	33.8	504	4	US-09-217-345-4	Sequence 4, Appli
36	912	33.8	504	4	US-09-892-985-4	Sequence 4, Appli
37	909.5	33.7	629	1	US-08-278-635B-6	Sequence 6, Appli
38	909.5	33.7	629	3	US-08-464-258B-6	Sequence 6, Appli
39	909.5	33.7	629	3	US-08-471-961-6	Sequence 6, Appli
40	909.5	33.7	629	4	US-09-345-109C-6	Sequence 6, Appli
41	898	33.2	497	1	US-08-278-635B-5	Sequence 5, Appli
42	898	33.2	497	3	US-08-464-258B-5	Sequence 5, Appli
43	898	33.2	497	3	US-08-471-961-5	Sequence 5, Appli
44	898	33.2	497	4	US-09-345-109C-5	Sequence 5, Appli
45	891	33.0	627	4	US-08-487-596-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-08-466-589-8
; Sequence 8, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-466-589-8

Query Match 100.0%; Score 2702; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-272;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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;
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-08-700-636-8

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Db	1	MRCSPGGVWMLAALASLHVSLOQGFQRLKYLKYNVNPPLRPVANDSQPLTVVFSLSLL	60
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Db	61	QIMDVDEKNOVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRFDPDQIWKPDILLYNSADE	120
QY	121	RFDATFTHTNVLVNSGHCQYLPPGIFKSSCYIDVRWPFDDVQHCCLKFGWSYSGWSL	180
Db	121	RFDATFTHTNVLVNSGHCQYLPPGIFKSSCYIDVRWPFDDVQHCCLKFGWSYSGWSL	180
QY	181	QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
Db	181	QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
QY	241	CVLSALALLVFLLPADSGEKISLIGITVLLSLTVFMLVAEIMPATSDVPLIAQYFAST	300
Db	241	CVLSALALLVFLLPADSGEKISLIGITVLLSLTVFMLVAEIMPATSDVPLIAQYFAST	300
QY	301	MIIVGLSVVTVIVLYQHHHPDGGKMPKTRVILLNWCANFLMKRPGEDKVRPACQHK	360
Db	301	MIIVGLSVVTVIVLYQHHHPDGGKMPKTRVILLNWCANFLMKRPGEDKVRPACQHK	360
QY	361	QRCCLASVEMSAVAPPASNGNLLIYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHL	420
Db	361	QRCCLASVEMSAVAPPASNGNLLIYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHL	420
QY	421	LHGGOPPEGDDPLAKILEEVYIANRFRQDESEAVCSEWFAACVVDRLCLMAFSVFTI	480
Db	421	LHGGOPPEGDDPLAKILEEVYIANRFRQDESEAVCSEWFAACVVDRLCLMAFSVFTI	480
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RESULT 2

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US-08-700-636-8
; Sequence 8, Application US/08700636
; Patent No. 5910582
;
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9368
; TELECOMMUNICATION INFORMATION:

```

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;
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-08-700-636-8

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QY	1	MRCSPGGVWMLAALASLHVSLOQGFQRLKYLKYNVNPPLRPVANDSQPLTVVFSLSLL	60
Db	1	MRCSPGGVWMLAALASLHVSLOQGFQRLKYLKYNVNPPLRPVANDSQPLTVVFSLSLL	60
QY	61	QIMDVDEKNOVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRFDPDQIWKPDILLYNSADE	120
Db	61	QIMDVDEKNOVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRFDPDQIWKPDILLYNSADE	120
QY	121	RFDATFTHTNVLVNSGHCQYLPPGIFKSSCYIDVRWPFDDVQHCCLKFGWSYSGWSL	180
Db	121	RFDATFTHTNVLVNSGHCQYLPPGIFKSSCYIDVRWPFDDVQHCCLKFGWSYSGWSL	180
QY	181	QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
Db	181	QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
QY	241	CVLSALALLVFLLPADSGEKISLIGITVLLSLTVFMLVAEIMPATSDVPLIAQYFAST	300
Db	241	CVLSALALLVFLLPADSGEKISLIGITVLLSLTVFMLVAEIMPATSDVPLIAQYFAST	300
QY	301	MIIVGLSVVTVIVLYQHHHPDGGKMPKTRVILLNWCANFLMKRPGEDKVRPACQHK	360
Db	301	MIIVGLSVVTVIVLYQHHHPDGGKMPKTRVILLNWCANFLMKRPGEDKVRPACQHK	360
QY	361	QRCCLASVEMSAVAPPASNGNLLIYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHL	420
Db	361	QRCCLASVEMSAVAPPASNGNLLIYIGFRGLDGVHCVPTPDGSGVVCGRMACSPHDEHL	420
QY	421	LHGGOPPEGDDPLAKILEEVYIANRFRQDESEAVCSEWFAACVVDRLCLMAFSVFTI	480
Db	421	LHGGOPPEGDDPLAKILEEVYIANRFRQDESEAVCSEWFAACVVDRLCLMAFSVFTI	480
QY	481	ICTIGILMSAPNFVEAVSKDFA 502	
Db	481	ICTIGILMSAPNFVEAVSKDFA 502	

RESULT 3

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US-08-467-574-8
; Sequence 8, Application US/08467574
; Patent No. 6022704
;
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA: US/08/467,574
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9949
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-467-574-8

Query Match 100.0%; Score 2702; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-272; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRCSPGGVWLALAAASLLHVSLLQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGVWLALAAASLLHVSLLQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Qy 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGKTVRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGKTVRFPDQGIWKPDILLYNSADE 120
Qy 121 RFDAFTHTNLVNSSGHCQYLPFGIFKSSCYDVRWFFDVQHCCLKFSGWSYGSWLDL 180
Db 121 RFDAFTHTNLVNSSGHCQYLPFGIFKSSCYDVRWFFDVQHCCLKFSGWSYGSWLDL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRTLYGNNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRTLYGNNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 300
Qy 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKRPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKRPGEDKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPPTDGSVVCGRMACSPHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPPTDGSVVCGRMACSPHDEHL 420
Qy 421 LHGGOPPGDDPLAKILEVRYIANRFRQDESEAVCSFEMKFAACVVDRLCLIMAFSVFTI 480
Db 421 LHGGOPPGDDPLAKILEVRYIANRFRQDESEAVCSFEMKFAACVVDRLCLIMAFSVFTI 480
Qy 481 ICTGILMSAPNFVEAVSKDFA 502
Db 481 ICTGILMSAPNFVEAVSKDFA 502

RESULT 4

US-09-217-345-8
Sequence 8, Application US/09217345
Patent No. 6303753
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.

APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-217-345-8

Query Match 100.0%; Score 2702; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-272; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRCSPGGVWLALAAASLLHVSLLQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGVWLALAAASLLHVSLLQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Qy 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGKTVRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGKTVRFPDQGIWKPDILLYNSADE 120
Qy 121 RFDAFTHTNLVNSSGHCQYLPFGIFKSSCYDVRWFFDVQHCCLKFSGWSYGSWLDL 180
Db 121 RFDAFTHTNLVNSSGHCQYLPFGIFKSSCYDVRWFFDVQHCCLKFSGWSYGSWLDL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRTLYGNNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRTLYGNNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFAS 300
Qy 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKRPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKRPGEDKVRPACQHK 360

QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGMACSPHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGMACSPHDEHL 420
QY 421 LHGGOPPEGDPLAKILEVRVIANRFRCDSEAVCSEWKFACVWDLCLMAFSVFTI 480
DB 421 LHGGOPPEGDPLAKILEVRVIANRFRCDSEAVCSEWKFACVWDLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 5

US-08-487-596-12
; Sequence 12, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-487-596-12

Query Match

100.0%; Score 2702; DB 4; Length 502;

Best Local Similarity 100.0%; Pred. No. 1.4e-272;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRCSPGGWLAALASLLHVSLOGEFORKLYKELVKNYNPLRPPVANDSQPLTVVFSLSLL 60
DB 1 MRCSPGGWLAALASLLHVSLOGEFORKLYKELVKNYNPLRPPVANDSQPLTVVFSLSLL 60
QY 61 QIMVDENKQVLTNINLQMSWTDHYLQWNVSEYPGVKTFRFPDQGIWKPDIILYNSADE 120
DB 61 QIMVDENKQVLTNINLQMSWTDHYLQWNVSEYPGVKTFRFPDQGIWKPDIILYNSADE 120
QY 121 RFDATFTNVLNVSNGHCQYLPPIGFKSSCIDVVRWPPFDVQHCKLKEGWSYGSWSIDL 180
DB 121 RFDATFTNVLNVSNGHCQYLPPIGFKSSCIDVVRWPPFDVQHCKLKEGWSYGSWSIDL 180
QY 181 QMOEADISGYIPNGEWDLVGIPGKSERFECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
DB 181 QMOEADISGYIPNGEWDLVGIPGKSERFECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHDDPGGMPKTRVILLNWCANFLMKRPGEDKVRACQHK 360
DB 301 MIIVGLSVVTVIVLQYHHDDPGGMPKTRVILLNWCANFLMKRPGEDKVRACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGMACSPHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGMACSPHDEHL 420
QY 421 LHGGOPPEGDPLAKILEVRVIANRFRCDSEAVCSEWKFACVWDLCLMAFSVFTI 480
DB 421 LHGGOPPEGDPLAKILEVRVIANRFRCDSEAVCSEWKFACVWDLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 6
US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. 6664375
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Harpold, Michael M.
; Ellis, Steven B.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95

APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8

Query Match 100.0%; Score 2702; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-272; Indels 0; Gaps 0;
Matches 502; Conservative 0; Mismatches 0;

Qy	1	MRCSPGGVWMLAASLLHVSLSQGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL	60
Db	1	MRCSPGGVWMLAASLLHVSLSQGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL	60
Qy	61	QIMDVDEKQVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE	120
Db	61	QIMDVDEKQVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE	120
Qy	121	RPDFTHTNVLNVSNGHCQYLPFGIFKSSCYIDVRWFPFDVQVCKLFGSWSYGSWLSLDL	180
Db	121	RPDFTHTNVLNVSNGHCQYLPFGIFKSSCYIDVRWFPFDVQVCKLFGSWSYGSWLSLDL	180
Qy	181	QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
Db	181	QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
Qy	241	CVLISALALLVFLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS	300
Db	241	CVLISALALLVFLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS	300
Qy	301	MIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKRPGEDKVPACQHK	360
Db	301	MIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKRPGEDKVPACQHK	360
Qy	361	QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPSGVVCGMACSPTHDEHL	420
Db	361	QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPSGVVCGMACSPTHDEHL	420
Qy	421	LHGQPPGEGDPLAKILLEEVYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI	480
Db	421	LHGQPPGEGDPLAKILLEEVYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI	480
Qy	481	ICTIGILMSAPNFVEAVSKDFA 502	
Db	481	ICTIGILMSAPNFVEAVSKDFA 502	

RESULT 7
US-09-771-737-2
Sequence 2, Application US/08771737
Patent No. 6323000
GENERAL INFORMATION:
APPLICANT: Briggs, Clark A.
APPLICANT: Gopalakrishnan, Murali
APPLICANT: McKenna, David G.
APPLICANT: Monteggia, Lisa M.
APPLICANT: Roch, Jean-Marc
APPLICANT: Sullivan, James P.
APPLICANT: Touma, Edward

APPLICANT: Abbott Laboratories
TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
FILE REFERENCE: 6017 US.01
CURRENT APPLICATION NUMBER: US/08/771,737
CURRENT FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 502
TYPE: PRT
ORGANISM: homo sapien
US-08-771-737-2

Query Match 99.9%; Score 2698; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.7e-272; Indels 0; Gaps 0;
Matches 501; Conservative 0; Mismatches 1;

Qy	1	MRCSPGGVWMLAASLLHVSLSQGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL	60
Db	1	MRCSPGGVWMLAASLLHVSLSQGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL	60
Qy	61	QIMDVDEKQVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE	120
Db	61	QIMDVDEKQVLTNNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE	120
Qy	121	RPDFTHTNVLNVSNGHCQYLPFGIFKSSCYIDVRWFPFDVQVCKLFGSWSYGSWLSLDL	180
Db	121	RPDFTHTNVLNVSNGHCQYLPFGIFKSSCYIDVRWFPFDVQVCKLFGSWSYGSWLSLDL	180
Qy	181	QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
Db	181	QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP	240
Qy	241	CVLISALALLVFLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS	300
Db	241	CVLISALALLVFLPADSGEKISLGIITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS	300
Qy	301	MIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKRPGEDKVPACQHK	360
Db	301	MIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCANFLMKRPGEDKVPACQHK	360
Qy	361	QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPSGVVCGMACSPTHDEHL	420
Db	361	QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPSGVVCGMACSPTHDEHL	420
Qy	421	LHGQPPGEGDPLAKILLEEVYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI	480
Db	421	LHGQPPGEGDPLAKILLEEVYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI	480
Qy	481	ICTIGILMSAPNFVEAVSKDFA 502	
Db	481	ICTIGILMSAPNFVEAVSKDFA 502	

RESULT 8
US-09-954-936-2
Sequence 2, Application US/09954936
Patent No. 6683157
GENERAL INFORMATION:
APPLICANT: Briggs, Clark A.
APPLICANT: Gopalakrishnan, Murali
APPLICANT: McKenna, David G.
APPLICANT: Monteggia, Lisa M.
APPLICANT: Roch, Jean-Marc
APPLICANT: Sullivan, James P.
APPLICANT: Touma, Edward
APPLICANT: Abbott Laboratories
TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
FILE REFERENCE: 6017 US.01
CURRENT APPLICATION NUMBER: US/09/954,936
CURRENT FILING DATE: 2001-09-18

Wed May 12 09:51:14 2004

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; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-09-954-936-2

Query Match          99.9%; Score 2698; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.7e-272;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGWLAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGGWLAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSL 60

QY 61 QIMVDKKNQVLTNIWLQSWTDHYLQNVSEYPGKTVRPDPDQIWKPDILLYNSADE 120
DB 61 QIMVDKKNQVLTNIWLQSWTDHYLQNVSEYPGKTVRPDPDQIWKPDILLYNSADE 120

QY 121 RFDATEHTNVLNNSGHCQYLPPIKSSCYIDVRWPFDPVQHCCKLKFGSWSYGWSL 180
DB 121 RFDATEHTNVLNNSGHCQYLPPIKSSCYIDVRWPFDPVQHCCKLKFGSWSYGWSL 180

QY 181 QMEADISGVIENGEDLVGIPKRSERFVECKEYPDVTFTVTRRRRTLYYGLNLLIP 240
DB 181 QMEADISGVIENGEDLVGIPKRSERFVECKEYPDVTFTVTRRRRTLYYGLNLLIP 240

QY 241 CVLISALALVFLPADSGEKISIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALVFLPADSGEKISIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIIVGLSVVTVIVLVQHHHDPDGGKMPKTRVILLNCAWFLMRKRPGEKVKRPACQHK 360
DB 301 MIIIVGLSVVTVIVLVQHHHDPDGGKMPKTRVILLNCAWFLMRKRPGEKVKRPACQHK 360

QY 361 QRCSLASVMSAVAPPASGNLLYIGFRLDGVCHVCTPDPDGVVCGRMACSPTHDEHL 420
DB 361 QRCSLASVMSAVAPPASGNLLYIGFRLDGVCHVCTPDPDGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPEGPDLLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPEGPDLLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTGILMSAPNFVEAVSKDFA 502
DB 481 ICTGILMSAPNFVEAVSKDFA 502

RESULT 9
US-08-278-635B-7
; Sequence 7, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,635B
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-635B-7

Query Match          94.2%; Score 2544; DB 1; Length 502;
Best Local Similarity 93.8%; Pred. No. 4e-256;
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGVWLAALASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65
DB 6 GGVWLAALASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65

QY 66 DEKNQVLTNIWLQSWTDHYLQNVSEYPGKTVRPDPDQIWKPDILLYNSADERFAT 125
DB 66 DEKNQVLTNIWLQSWTDHYLQNVSEYPGKTVRPDPDQIWKPDILLYNSADERFAT 125

QY 126 FHTNVLNNSGHCQYLPPIKSSCYIDVRWPFDPVQHCCKLKFGSWSYGWSLQMQEA 185
DB 126 FHTNVLNNSGHCQYLPPIKSSCYIDVRWPFDPVQHCCKLKFGSWSYGWSLQMQEA 185

QY 186 DISGYIPNGEWDLVGIPKRSERFVECKEYPDVTFTVTRRRRTLYYGLNLLIPCVLIS 245
DB 186 DISGYIPNGEWDLVGIPKRSERFVECKEYPDVTFTVTRRRRTLYYGLNLLIPCVLIS 245

QY 246 ALALLYFLPADSGEKISIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
DB 246 ALALLYFLPADSGEKISIGITVLLSLTFVLLVAEIMPATSDSVPLIAQYFASTMIIVG 305

QY 306 LSVVVTVIVLVQHHHDPDGGKMPKTRVILLNCAWFLMRKRPGEKVKRPACQHKRRC 365
DB 306 LSVVVTVIVLVQHHHDPDGGKMPKTRVILLNCAWFLMRKRPGEKVKRPACQHKRRC 365

QY 366 LASVMSAVAPPASGNLLYIGFRLDGVCHVCTPDPDGVVCGRMACSPTHDEHLHGQ 425
DB 366 LASVMSAVAPPASGNLLYIGFRLDGVCHVCTPDPDGVVCGRMACSPTHDEHLHGQ 425

QY 426 PPSGDDPLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTICTIG 485
DB 426 PPSGDDPLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTICTIG 485

QY 486 ILMSAPNFVEAVSKDFA 502
DB 486 ILMSAPNFVEAVSKDFA 502

RESULT 10
US-08-464-258B-7
; Sequence 7, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
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Db 49 QIMDVDEKQV--TTNIW-QMSWDHY-QMNVSEYPGVKTFRFPDQIWKPD1--YNSADE 103
Qy 121 RFDATEFTNVLNSSGHCQVLPFGIFKSSCYIDVRWPFDDVOHCKLFGSWSYGGWLDL 180
Db 104 RFDATEFTNV-VNSSGHCQV-PPGIFKSSCYIDVRWPFDDVOHCK-KFGSWSYGGWS--D 158
Qy 181 QMOBADI SGYPNGEWDLVGPGRKSRFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 240
Db 159 QMOBADI SGYPNGEWDLVGPGRKSRFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIP 213
Qy 241 CVLISALALLVFLPADSGEKISIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 214 CVISAA-----VFPADSGEKIS-GITV---STVFM---VAEIMPATSDSVPLIAQYFAS 260
Qy 301 MIIVGLSVVTVIYVQHHDDPDGGRKMPKTRVILLNWCWFLRMKPGEDKVRPACQHK 360
Db 261 MIIVGLSVVTVIYVQHHDDPDGGRKMPKTRVILLNWCWFLRMKPGEDKVRPACQHK 315
Qy 361 QRRCSLASVMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSDGVVCGRMACSPTHDEHL 420
Db 316 QRRCS--ASVMSAVAPPASNGN--YIGFRG-DGVHCVPTPDSDGVVCGRMACSPTHDEH- 370
Qy 421 LHGOQPEGDDLAKEVEVYIANRFRCDSEAVCSEWKFACCVDRCLCMAFSVFTI 480
Db 371 -HGOQPEGDD-KEI-EVRYIANRFRCDSEAVCSEWKFACCVDR--CNAFSVFTI 425
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 426 ICTIGI-MSAPNFVEAVSKDFA 446

RESULT 14
US-08-278-635B-8
; Sequence 8, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278, 635B
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-278-635B-8
Query Match 67.4%; Score 1820.5; DB 1; Length 511;
Best Local Similarity 69.0%; Pred. No. 9.5e-181;
Matches 343; Conservative 56; Mismatches 93; Indels 5; Gaps 4;
Qy 8 VMLAASLLHVSLOGEFQKLYKELVKNVNPILPVPVANDSQPLTVVFSLSLQIMDVDE 67
Db 16 LWSLFLSPFKVQSQESQRLRYDLNLTNRLRPLPVPVANDSQPLTVVFSLSLQIMDVDE 75
Qy 68 KNOVLITNIMLQSWTDHYLQNVSEYPGVKTFRFPDQIWKPD1LLYNSADREFDATEH 127
Db 76 KNOVLITNIMLQSWTDHYLQNVSEYPGVKTFRFPDQIWKPD1LLYNSADREFDATEH 135
Qy 128 TNVLNSSGHCQVLPFGIFKSSCYIDVRWPFDDVOHCKLFGSWSYGGWLDLQMOBADI 187
Db 136 TNVLNSSGHCQVLPFGIFKSSCYIDVRWPFDDVOHCKLFGSWSYGGWLDLQMOBADI 195
Qy 188 SGYPNGEWDLVGPGRKSRFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIPCVLISAL 247
Db 196 SNTYISNGEWDLVGPGRKSRFYECCKEPYDPDVTFTVMRRRTLYYGLNLLIPCVLISGL 255
Qy 248 ALLVFLPADSGEKISIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASIMVIGLS 307
Db 256 ALLVFLPADSGEKISIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASIMVIGLS 315
Qy 308 VVTVIYVQHHDDPDGGRKMPKTRVILLNWCWFLRMKPGEDKVRP-ACQHK--QRRC 364
Db 316 VVTVIYVQHHDDPDGGRKMPKTRVILLNWCWFLRMKPGEDKVRP-ACQHK--QRRC 374
Qy 365 SLASVMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSDGVVCGRMACSPTHDEHLGG 424
Db 375 SLKXNTNNVLPFGHQSNGNMIY-SYHTMENPCCPQNNDLGSKSGKITCPLSEDNEHVQKK 433
Qy 425 QPPEGDDLAKEVEVYIANRFRCDSEAVCSEWKFACCVDRCLCMAFSVFTI 484
Db 434 ALMDTIPVIVKILEVQFIAMRFKQDEGEICSEWKFACCVDRCLCMAFSVFTI 493
Qy 485 GILMSAPNFVEAVSKDFA 501
Db 494 TILMSAPNFVEAVSKDFA 510

RESULT 15
US-08-464-258B-8
; Sequence 8, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464, 258B
; FILING DATE: 06/05/95
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278, 635

Wed May 12 09:51:14 2004

Search completed: May 5, 2004, 15:32:37
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: May 5, 2004, 15:23:27 ; Search time 60 Seconds
(without alignments)
2363.981 Million cell updates/sec

Title: US-09-703-951a-12
Perfect score: 2702
Sequence: 1 MRCSPGGVWLALASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Genesecp1980s:*
2: Genesecp1990s:*
3: Genesecp2000s:*
4: Genesecp2001s:*
5: Genesecp2002s:*
6: Genesecp2003as:*
7: Genesecp2003bs:*
8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2702	100.0	502	2 AAW44153	Aaw44153 Human neu
2	2702	100.0	502	2 AAW09025	Aaw09025 Neuronal
3	2702	100.0	502	3 AAB24088	Aab24088 Human PRO
4	2702	100.0	502	4 AAB82690	Aab82690 Nicotinic
5	2702	100.0	502	4 AAB50012	Aab50012 Wild-type
6	2702	100.0	502	5 AABG70492	Abg70492 Human neu
7	2702	100.0	502	5 ABB82435	Abb82435 Human neu
8	2702	100.0	502	7 ADA10874	Ada10874 Human neu
9	2702	100.0	502	7 ADD47051	Add47051 Human PRO
10	2702	100.0	502	7 ADE57310	Ade57310 Human PRO
11	2698	99.9	502	2 AAW69216	Aaw69216 V274T var
12	2696	99.8	502	4 AAB50015	Aab50015 Mutant hu
13	2692	99.6	502	4 AAB50016	Aab50016 Mutant hu
14	2686	99.4	502	4 AAB50017	Aab50017 Mutant hu
15	2535	93.8	502	7 ADE57308	Ade57308 Rat Prote
16	2535	93.8	502	7 ADD47049	Add47049 Rat Prote
17	2433	90.0	502	2 AAW12368	Aaw12368 Neuronal
18	2026	75.0	446	7 ADA10865	Ada10865 Human neu
19	1820.5	67.4	511	2 AAW12369	Aaw12369 Neuronal
20	1794	66.4	349	5 AABP69081	Abp69081 Human pol
21	1478.5	54.7	470	4 AAB50014	Aab50014 Chimeric
22	1364.5	50.5	448	4 AAB50018	Aab50018 Mature ce
23	1258.5	46.6	501	3 AAY50816	Aay50816 H. viresc
24	1246	46.1	496	3 AAY50815	Aay50815 H. viresc
25	1159.5	42.9	770	3 AAY50814	Aay50814 D. melano

ALIGNMENTS									
RESULT 1									
AAW44153									
ID	AAW44153	standard; protein; 502 AA.							
XX	AAW44153;								
AC	AAW44153;								
DT	14-MAY-1998	(first entry)							
XX									
DE		Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.							
XX									
KW		Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;							
KM		brain tissue; screening; NACHR; antibody.							
XX									
OS		Homo sapiens.							
XX									
FH	Key	Location/Qualifiers							
FT	Peptide	1..23							
FT	Domain	/label= signal							
FT		229..256							
FT		/label= TMD1							
FT		/note= "transmembrane domain"							
FT		262..284							
FT		/label= TMD2							
FT		/note= "transmembrane domain"							
FT		290..317							
FT		/label= TMD3							
FT		/note= "transmembrane domain"							
FT		318..461							
FT		/label= cytoplasmic_loop							
FT	Misc-difference	343							
FT		/note= "encoded by CTS"							
FT		462..487							
FT		/label= TMD4							
FT		/note= "transmembrane domain"							
XX									
XX		WO9420617-A2.							
XX									
PD		15-SEP-1994.							
XX									
XX		08-MAR-1994; 94WO-US002447.							
XX									
XX		08-MAR-1993; 93US-00028031.							
XX									
PA		(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.							
XX									
PI		Elliot KJ, Ellis SB, Harpold MM;							
XX									
DR		WPI; 1994-303024/37.							

Aae12824 Caenorhab
Abp96318 Caenorhab
Aao17243 Modified
Aao17245 Modified
Abb08885 Modified
Abb63683 Drosophil
Aaw44155 Human neu
Aar73966 Alpha 2 s
Aaw09021 Neuronal
Abg61850 Prostate
Abg31800 Human neu
Abb82430 Human neu
Ada10855 Human neu
Adc71171 Human 205
Adc71169 Human 205
Add45584 Human PRO
Ade59169 Human PRO
Aao17242 Modified
Abb08883 Insect ni
Abb61954 Drosophil

DR N-PSDB; AAV12197.
 XX Human neuronal nicotinic acetylcholine receptor subunits and DNA - also
 PT transformed cells useful for screening cpds. which modulate activity of
 PT the receptor.
 XX
 XX
 PS Claim 7; Page 80-81; 99pp; English.
 XX
 CC The present sequence represents a human neuronal nicotinic acetylcholine
 CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
 CC NACHR subunits may be used in a method of screening compounds to identify
 CC any which modulate the activity of human neuronal NACHR. Subunit specific
 CC antibodies may be used to monitor the distribution and expression density
 CC of various subunits in normal vs diseased brain tissues. Testing of
 CC single receptor subunits or specific receptor subunit combinations with a
 CC variety of potential agonists or antagonists provides information with
 CC respect to the function and activity of the individual subunits and
 CC should lead to the identification and design of compounds that are
 CC capable of very specific interaction with one or more receptor subtypes.
 CC The resulting drugs should exhibit fewer unwanted side effects than drugs
 CC identified e.g. screening with cells that express a variety of subtypes
 XX
 SQ Sequence 502 AA;

Query Match 100.0%; Score 2702; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 6.9e-264;
 Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGWVLAASLLHVSLOGEQRKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGWVLAASLLHVSLOGEQRKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKNQVLTNNILQMSWTDHYLQWNVSEYGVKTVRFPDQGIWKPDI 120
 DB 61 QIMDVDEKNQVLTNNILQMSWTDHYLQWNVSEYGVKTVRFPDQGIWKPDI 120
 QY 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHKLFKGSW 180
 DB 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHKLFKGSW 180
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 DB 181 QMGEADISGYIPNGEWDLVGIPGKSERFEYCKEPEYDVTFTVTRRTLY 240
 QY 241 CVLISALALLVFLPADSGEKISLGTIVLLSLTVFMLLVAEIMPATSDSV 300
 DB 241 CVLISALALLVFLPADSGEKISLGTIVLLSLTVFMLLVAEIMPATSDSV 300
 QY 301 MIIVGLSVVTVTVILQYHHDDPGGKMPKWTTRVILLNWCAMFLRMKRP 360
 DB 301 MIIVGLSVVTVTVILQYHHDDPGGKMPKWTTRVILLNWCAMFLRMKRP 360
 QY 361 QRCISLASVEMSAVAPPPASNGNLVIGRGLDGVHCVTPTDPSGVVCG 420
 DB 361 QRCISLASVEMSAVAPPPASNGNLVIGRGLDGVHCVTPTDPSGVVCG 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANFRFCQDESEAVCSWKFAACVVDRL 480
 DB 421 LHGGQPPGDPDLAKILEEVRYIANFRFCQDESEAVCSWKFAACVVDRL 480
 QY 481 ICTIGILMSAPNFEAVSKDFA 502
 DB 481 ICTIGILMSAPNFEAVSKDFA 502

RESULT 2

AAW09025
 ID AAW09025 standard; protein; 502 AA.
 XX
 AC AAW09025;
 XX
 DT 09-APR-1997 (first entry)
 XX

DE Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
 XX
 KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 KW ligand-gated receptor.
 XX
 OS Homo sapiens.
 XX
 PN MO9641876-A1.
 XX
 PD 27-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009775.
 XX
 PR 07-JUN-1995; 95US-00484722.
 XX
 PA (STBI-) SIBIA NEUROSCIENCES INC.
 XX
 FI Elliott KJ, Harpold MM;
 XX
 DR WPI; 1997-065463/06.
 XX
 DR N-PSDB; AAT48239.
 XX
 PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units - used
 PT in screening to determine the effect of drugs on the receptor.
 XX
 PS Disclosure; Page 73-74; 108pp; English.
 XX
 CC The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
 CC acetylcholine receptor (nAChR) can be expressed in transformed host cells
 CC carrying alpha-7 subunit DNA (see also AAT48239). Host cells, esp.
 CC mammalian cells or amphibian oocytes, expressing the recombinant alpha-7
 CC subunit, opt. in combination with other recombinant alpha and/or beta
 CC subunits (see also AAW09018-24, AAW09026-27), can be used to examine the
 CC function of human AChR and to identify cpds. that modulate its activity
 XX
 SQ Sequence 502 AA;

Query Match 100.0%; Score 2702; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 6.9e-264;
 Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGWVLAASLLHVSLOGEQRKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGWVLAASLLHVSLOGEQRKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKNQVLTNNILQMSWTDHYLQWNVSEYGVKTVRFPDQGIWKPDI 120
 DB 61 QIMDVDEKNQVLTNNILQMSWTDHYLQWNVSEYGVKTVRFPDQGIWKPDI 120
 QY 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHKLFKGSW 180
 DB 121 RPDATFHTNVLVNSGHCQYLPPIGPKSSCYIDVRWFFPDVQHKLFKGSW 180
 QY 181 QMGEADISGYIPNGEWDLVGIPGKSERFEYCKEPEYDVTFTVTRRTLY 240
 DB 181 QMGEADISGYIPNGEWDLVGIPGKSERFEYCKEPEYDVTFTVTRRTLY 240
 QY 241 CVLISALALLVFLPADSGEKISLGTIVLLSLTVFMLLVAEIMPATSDSV 300
 DB 241 CVLISALALLVFLPADSGEKISLGTIVLLSLTVFMLLVAEIMPATSDSV 300
 QY 301 MIIVGLSVVTVTVILQYHHDDPGGKMPKWTTRVILLNWCAMFLRMKRP 360
 DB 301 MIIVGLSVVTVTVILQYHHDDPGGKMPKWTTRVILLNWCAMFLRMKRP 360
 QY 361 QRCISLASVEMSAVAPPPASNGNLVIGRGLDGVHCVTPTDPSGVVCG 420
 DB 361 QRCISLASVEMSAVAPPPASNGNLVIGRGLDGVHCVTPTDPSGVVCG 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANFRFCQDESEAVCSWKFAACVVDRL 480
 DB 421 LHGGQPPGDPDLAKILEEVRYIANFRFCQDESEAVCSWKFAACVVDRL 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3
AAB24088
ID AAB24088 standard; protein; 502 AA.
XX
AC AAB24088;

XX 29-JAN-2001 (first entry)
XX Human PRO2145 protein sequence SEQ ID NO:77.

XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macropagal disorder;
KW epithelial disorder; stromal disorder; blastocoelec disorder;
KW inflammatory disorder; immunologic disorder.

XX Homo sapiens.

OS WO200053755-A2.

PN 14-SEP-2000.

PD 06-JAN-2000; 2000WO-US0000376.

XX 08-MAR-1999; 99WO-US0005028.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 07-JUL-1999; 99US-0143048P.

PR 26-JUL-1999; 99US-0145698P.

PR 30-NOV-1999; 99WO-US028313.

PR 20-DEC-1999; 99WO-US030911.

PR 05-JAN-2000; 2000WO-US000219.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WI;
PI WPI; 2000-572270/53.
XX N-PSDB; AAC58395.

XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer.

XX Claim 61; Fig 58; 286pp; English.

XX The present invention describes an isolated antibody that binds to one of
CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,
CC PRO717, PRO809, PRO848, PRO943, PRO1005, PRO1009, PRO1025,
CC PRO1030, PRO1097, PRO1107, PRO1153, PRO1182, PRO1184, PRO1187,
CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR
CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The
CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis
CC and prevention of cancer. The antibodies and other anti-tumour compounds
CC maybe used to treat various conditions, including those characterised by
CC overexpression and/or activation of the amplified PRO genes. Exemplary
CC conditions or disorders to be treated with such antibodies and other
CC compounds include benign or malignant tumours (e.g., renal, liver,
CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,
CC glioblastomas, and various head and neck tumours), leukaemias and
CC lymphoid malignancies, other disorders such as neuronal, glial,
CC astrocytal, hypothalamic and other glandular, macropagal, epithelial,
CC stromal and blastocoelec disorders, and inflammatory, angiogenic and
CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and

CC hybridisation probes used in the isolation of the human PRO sequences.
CC AAC58367 to AAC58396 and AAC24057 to AAC24089 represent human PRO
CC polynucleotide and protein sequences given in the exemplification of the
CC present invention
XX
SQ Sequence 502 AA;

Query Match 100.0%; Score 2702; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 6.9e-264;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALAAASLLHVSLLQGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSLSL 60
DB 1 MRCSPGGVWLAALAAASLLHVSLLQGEFQKLYKELVKNYNPLERPVANDSOPLTVYFSLSL 60

QY 61 QIMDVDEKNQVLTITNIMLQMSWTDLHYNVSEYFGVKTVPFDDGQIMKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTITNIMLQMSWTDLHYNVSEYFGVKTVPFDDGQIMKPDILLYNSADE 120

QY 121 RFDATFHTNVLVNSGHCQYLPPIFKSSCYIDVRFPPDVQVCKLKFGSWYGGWSLDL 180
DB 121 RFDATFHTNVLVNSGHCQYLPPIFKSSCYIDVRFPPDVQVCKLKFGSWYGGWSLDL 180

QY 181 QMOEADISGVIENGWDIAGVIGKSEFEYCKEPEYDVTFVTMRRRTLYVGNLLIP 240
DB 181 QMOEADISGVIENGWDIAGVIGKSEFEYCKEPEYDVTFVTMRRRTLYVGNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFVMLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFVMLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTIVILLNWCAPLEMKERGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQYHHDDPGGKMPKWTIVILLNWCAPLEMKERGEDKVRPACQHK 360

QY 361 QRCESLASVEMSAVAPPASNGNLLYIGRGLDGVHCVTPTDPSGVVCGMACSPTHDEHL 420
DB 361 QRCESLASVEMSAVAPPASNGNLLYIGRGLDGVHCVTPTDPSGVVCGMACSPTHDEHL 420

QY 421 LHGGQPPGPDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPGPDPLAKILEEVRYIANFRQDSEAVCSWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502

DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4
AAB82690
ID AAB82690 standard; protein; 502 AA.

XX AAB82690;

XX 15-OCT-2001 (first entry)

XX Nicotinic acetylcholine receptor alpha7.

XX Nicotinic acetylcholine receptor; nAChR; human;
KW acetylcholine binding protein; AChBP; mollusc; ligand-binding protein;
KW ligand-gated ion channel; crystal; drug design; protein co-ordinates data;
KW schizophrenia; Alzheimer's disease; nicotine addiction;
KW Tourette's syndrome; therapy; neurotropic; neuroprotective.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Region 108..115
FT /note= "conserved ligand-binding region, residues Trp108
FT and Tyr115 are essential"

XX Region 171..173
FT /note= "conserved ligand-binding region, residues Trp171
FT and Tyr173 are essential"

Qy	61	QIMDVDEKNQVLTNNIWMQSWTDHYLQWNVSEYFGVKTVPDPDQGIWKPDILLYNSADE	120
Db	61	QIMDVDEKNQVLTNNIWMQSWTDHYLQWNVSEYFGVKTVPDPDQGIWKPDILLYNSADE	120
Qy	121	RFDATEHTNNVLVNSGHCQYLPGGIHFJKSSCYIDVRWFPPDVQCHLKFQSGWSYGWSLDL	180
Db	121	RFDATEHTNNVLVNSGHCQYLPGGIHFJKSSCYIDVRWFPPDVQCHLKFQSGWSYGWSLDL	180
Qy	181	QMQEADISGYIPNGEWDVLVGIPIGKRSERFYECCKEPPYPOVTVTVMRRRTLYYGLNLLIP	240
Db	181	QMQEADISGYIPNGEWDVLVGIPIGKRSERFYECCKEPPYPOVTVTVMRRRTLYYGLNLLIP	240
Qy	241	CVLISALALLVFLIPADSGEKISLGI TVLLSLTVFMLLVAEIMPATSDSVPLIAQVFAST	300
Db	241	CVLISALALLVFLIPADSGEKISLGI TVLLSLTVFMLLVAEIMPATSDSVPLIAQVFAST	300
Qy	301	MIIVGLSVVVTVIQLQYHHDDPGGKMPKWTRVILLNWC AFLRMKRPCEGKV RPACQHK	360
Db	301	MIIVGLSVVVTVIQLQYHHDDPGGKMPKWTRVILLNWC AFLRMKRPCEGKV RPACQHK	360
Qy	361	QRRCSLASVMSAVAPPASNGNLLIYIGPRGLDGVHCVETPDPSGVVCGRMASCPTHDEHL	420
Db	361	QRRCSLASVMSAVAPPASNGNLLIYIGPRGLDGVHCVETPDPSGVVCGRMASCPTHDEHL	420
Qy	421	LHGGOPPGDPLAKILREVRVIANFRQDSEAVCESEWKFAACVVVDRLCLMAFVSFTI	480
Db	421	LHGGOPPGDPLAKILREVRVIANFRQDSEAVCESEWKFAACVVVDRLCLMAFVSFTI	480
Qy	481	ICTTIGILMSAPNFVEAVSKDFA 502	
Db	481	ICTTIGILMSAPNFVEAVSKDFA 502	

RESULT 6	
ABG70492	
ID	ABG70492 standard; protein; 502 AA.
XX	
AC	ABG70492;
XX	
DT	06-DEC-2002 (first entry)
XX	
DE	Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
XX	
KW	Human; neuronal nicotinic acetylcholine receptor; nNACHR; receptor;
KW	ion flux; alpha 7 subunit.
XX	
OS	Homo sapiens.
XX	
FN	US6440681-B1.
XX	
PD	27-AUG-2002.
XX	
PF	07-JUN-1995; 95US-00487596.
XX	
PR	03-APR-1990; 90US-00504455.
PR	30-NOV-1992; 92US-00938154.
PR	08-MAR-1993; 93US-00028031.
PR	08-NOV-1993; 93US-00149503.
XX	
PA	(MERI) MERCK & CO INC.
XX	
PI	Elliott KJ, Ellis SB, Harpold MM;
XX	
DR	WPI; 2002-711528/77.
DR	N-PSDB; ABS54875.
XX	
PT	Identifying antagonists or agonists of human neuronal nicotinic
PT	acetylcholine receptors, by contacting recombinant cells with test
PT	compound, and measuring ion flux of cells or binding of compound to
PT	nNACHR.
XX	
PS	Claim 101; Col 59-64; 56pp; English.
XX	

CC	The invention relates to a method for identifying compounds that are	
CC	agonists or agonists of human neuronal nicotinic acetylcholine	
CC	receptors (nAChRs), by contacting recombinant cells with a test compound	
CC	and measuring ion flux, the electrophysiological response of the cells or	
CC	binding of the test compound to the nAChR. The recombinant cells are	
CC	produced by transfection with a nucleic acid encoding at least one human	
CC	nAChR (alpha or beta) subunit, such that the cells express an nAChR	
CC	comprising one human subunit encoded by the transfected nucleic acid.	
CC	This sequence represents the alpha 7 subunit of the human nAChR	
CC	polypeptide	
CC		
XX	Sequence 502 AA;	
SQ		
	Query Match	100.0%; Score 2702; DB 5; Length 502;
	Best Local Similarity	100.0%; Pred. No. 6.9e-264;
	Matches 502; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MRCSPGGVTLAALASLIHVSLSQGFQKLYKELVKNYNPLRPVANDSQPIIVFSL	60
DB	1 MRCSPGGVTLAALASLIHVSLSQGFQKLYKELVKNYNPLRPVANDSQPIIVFSL	60
QY	61 QIMDVDEKNQVLTNIWLQMSWTDHYLQNNVSEYPGVKTVPFDDGQIWKPDILLNSADE	120
DB	61 QIMDVDEKNQVLTNIWLQMSWTDHYLQNNVSEYPGVKTVPFDDGQIWKPDILLNSADE	120
QY	121 RFDATFTNVLVNSGHCQYLPPIGKFSKCYIDVRWFDDVQHCCLKFSGWSYGGWSLDL	180
DB	121 RFDATFTNVLVNSGHCQYLPPIGKFSKCYIDVRWFDDVQHCCLKFSGWSYGGWSLDL	180
QY	181 QMQADISGYIPNGEWDLVGIPGKRSEFYECCKEYIPDVFTVTMRRTLYYGLNLLIP	240
DB	181 QMQADISGYIPNGEWDLVGIPGKRSEFYECCKEYIPDVFTVTMRRTLYYGLNLLIP	240
QY	241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST	300
DB	241 CVLISALALLVFLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST	300
QY	301 MIIVGLSVTVTVIYLYHHDPDGGKMPKWTIVLLNWCANFLRMKRPGEDKVRPACQHK	360
DB	301 MIIVGLSVTVTVIYLYHHDPDGGKMPKWTIVLLNWCANFLRMKRPGEDKVRPACQHK	360
QY	361 QRRCSLASVEMSAVAPPASNGNLIYIGFRGLDGVCVPTPDGSGVVCGRMACSPTHDEHL	420
DB	361 QRRCSLASVEMSAVAPPASNGNLIYIGFRGLDGVCVPTPDGSGVVCGRMACSPTHDEHL	420
QY	421 LHGGQPPGDPDLAKILBEVRYIANRFRQDESEAVCSWKFAACVWDELCLMAFSVFTI	480
DB	421 LHGGQPPGDPDLAKILBEVRYIANRFRQDESEAVCSWKFAACVWDELCLMAFSVFTI	480
QY	481 ICTIGILMSAPNFVEAVSKDFA 502	
DB	481 ICTIGILMSAPNFVEAVSKDFA 502	
RESULT 7		
ABB82435		
ID	ABB82435 standard; protein; 502 AA.	
XX		
AC	ABB82435;	
XX		
DT	22-JAN-2003 (first entry)	
XX		
DE	Human neuronal NACHr alpha7 subunit.	
XX		
KW	Human; neuronal; nicotinic acetylcholine receptor; NACHr; drug screening;	
XX	immunochemistry; NACHr alpha7 subunit; receptor.	
OS	Homo sapiens.	
XX		
PN	WO200259266-A2.	
XX		
PD	01-AUG-2002.	

PF	29-OCT-2001; 2001WO-US050985.	RESULT 8	
XX	01-NOV-2000; 2000US-00703951.	ADAL0874	
XX	(MERI) MERCK & CO INC.	ID	ADAL0874 standard; protein; 502 AA.
XX	Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;	AC	ADAL0874;
XX	WPI; 2002-698532/75.	DE	06-NOV-2003 (first entry)
DR	N-PSDB; ABV73248.	DT	Human neuronal nicotinic acetylcholine receptor alpha 7 subunit #1.
XX	Cell comprising nucleic acids encoding human alpha and beta subunits of	XX	alpha 7 subunit; human; neuronal nicotinic acetylcholine receptor;
XX	neuronal nicotinic acetylcholine receptors, useful for in vitro screening	KW	ligand-gated ion channel; synaptic transmission; gene therapy;
PT	of a drug substance in a test system specific for humans.	KW	transgenic; receptor.
PT		XX	Homo sapiens.
XX	Example; Page 130-131; 143pp; English.	OS	US6524789-B1.
XX	The invention relates to a suitable host cell transfected with an	XX	25-FEB-2003.
CC	isolated nucleic acid molecule comprising a sequence of nucleotides or	PD	07-JUN-1996; 96US-00660451.
CC	ribonucleotides that encodes at least one alpha or beta subunit of a	PF	07-JUN-1995; 95US-00484722.
CC	human neuronal nicotinic acetylcholine receptor (NACHR). The compositions	XX	(MERI) MERCK & CO INC.
CC	and methods of the present invention, which provide a means to prepare	XX	Elliott KJ, Harpold MM;
CC	synthetic or recombinant receptors and receptor subunits that are	XX	WPI; 2003-511917/48.
CC	substantially free of contamination from many other receptor proteins,	DR	N-PSDB; ADAL0864.
CC	are useful for observing the effect of a drug substance on a particular	XX	New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human
CC	subtype to perform in vitro screening of the drug substance in a test	PT	neuronal nicotinic acetylcholine receptor (NACHR), useful for identifying
CC	system that is specific for humans. The antibodies can be used in	PT	compounds that modulate human neuronal nACHR activity.
CC	immunohistochemistry and for diagnostic and therapeutic applications. The	XX	Disclosure; Col 67-72; 63pp; English.
CC	present sequence represents a human neuronal NACHR alpha7 subunit	XX	The invention relates to an isolated nucleic acid molecule comprising a
XX	Sequence 502 AA;	CC	nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human
Query Match	100.0%; Score 2702; DB 5; Length 502;	CC	neuronal nicotinic acetylcholine receptor NACHR. NACHR's form ligand-
Best Local Similarity	100.0%; Pred. No. 6.9e-264;	CC	gated ion channels that mediate synaptic transmissions between nerve and
Matches 502; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	CC	muscle and between neurons upon interaction with the neurotransmitter
QY	1 MRCSPGGWMLAALSHVSLQGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60	CC	acetylcholine. The nucleic acid molecule is useful for identifying
Db	1 MRCSPGGWMLAALSHVSLQGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60	CC	compounds that modulate human neuronal NACHR. The present sequence
QY	61 QIMDVEKQVLTNTNWLQMSWDHYLQWNVSEYPGVKTVPDGIWKPDILLYNSADE 120	CC	represents the amino acid sequence of the human neuronal nicotinic
Db	61 QIMDVEKQVLTNTNWLQMSWDHYLQWNVSEYPGVKTVPDGIWKPDILLYNSADE 120	CC	acetylcholine receptor, NACHR, alpha 7 subunit #1. Note: the present
QY	121 RFDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWFPFDVQHCCLKFSGWSYGLSL 180	CC	sequence is the sequence encoded by the NACHR alpha 7 subunit DNA
Db	121 RFDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWFPFDVQHCCLKFSGWSYGLSL 180	CC	ADAL0864.
QY	181 QMQEADISGYIPNGEWDLVGIPGRSRRFYECCKEYPDVTFTVWRRRTLYYGLNLLIP 240	XX	Sequence 502 AA;
Db	181 QMQEADISGYIPNGEWDLVGIPGRSRRFYECCKEYPDVTFTVWRRRTLYYGLNLLIP 240	Query Match	100.0%; Score 2702; DB 7; Length 502;
QY	241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFAS 300	Best Local Similarity	100.0%; Pred. No. 6.9e-264;
Db	241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTVFMLVAEIMPATSDSVPLIAQYFAS 300	Matches 502; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	301 MIIIVGLSVVTVIVLYQHHDDPDGCKMPKWTTRVILLNWCANFLMKRPGEDKVRPACQHK 360	QY	1 MRCSPGGWMLAALSHVSLQGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60
Db	301 MIIIVGLSVVTVIVLYQHHDDPDGCKMPKWTTRVILLNWCANFLMKRPGEDKVRPACQHK 360	Db	1 MRCSPGGWMLAALSHVSLQGEFQKLYKELVKNYNPLRPVANDSPLTVYFSLSL 60
QY	361 QRRCSLASVMSAVAPPASNGNLLYIGFRLDGVHCVPPTDSDVGVGCMACSPTHDEHL 420	QY	61 QIMDVEKQVLTNTNWLQMSWDHYLQWNVSEYPGVKTVPDGIWKPDILLYNSADE 120
Db	361 QRRCSLASVMSAVAPPASNGNLLYIGFRLDGVHCVPPTDSDVGVGCMACSPTHDEHL 420	Db	61 QIMDVEKQVLTNTNWLQMSWDHYLQWNVSEYPGVKTVPDGIWKPDILLYNSADE 120
QY	421 LHGQOPPEGDPDLAKILEEVYIANRRCQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480	QY	121 RFDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWFPFDVQHCCLKFSGWSYGLSL 180
Db	421 LHGQOPPEGDPDLAKILEEVYIANRRCQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480	Db	121 RFDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWFPFDVQHCCLKFSGWSYGLSL 180
QY	481 ICTIGILMSAPNFVEAVSKDFA 502	QY	181 QMQEADISGYIPNGEWDLVGIPGRSRRFYECCKEYPDVTFTVWRRRTLYYGLNLLIP 240
Db	481 ICTIGILMSAPNFVEAVSKDFA 502	Db	181 QMQEADISGYIPNGEWDLVGIPGRSRRFYECCKEYPDVTFTVWRRRTLYYGLNLLIP 240

Db 241 CVLISALALLVLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTAVILLNWCANFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTAVILLNWCANFLRMKRPGEKVRPACQHK 360
Qy 361 QRCRSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Db 361 QRCRSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 9
ID ADD47051 standard; protein; 502 AA.
XX ADD47051;
AC ADD47051;
XX 29-JAN-2004 (first entry)
XX Human Protein NP_000737, SEQ ID NO 12739.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; NP_000737.
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIFO at
CC ftp.wifo.int/pub/published_pct_sequences.
XX
SQ Sequence 502 AA;

Query Match 100.0%; Score 2702; DB 7; Length 502;
Best Local Similarity 100.0%; Pred. No. 6.9e-264;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRCSPGGVWLAAASLLHVSLSQGEFQKLYKELVKNYNPLERPVANOSPLTVYFSLSL 60
Db 1 MRCSPGGVWLAAASLLHVSLSQGEFQKLYKELVKNYNPLERPVANOSPLTVYFSLSL 60
Qy 61 QIMVDDEKQVLTINILQMSWTDHYLQNNVSEYGVKTVRPDGOIKWPDILLYNSADE 120
Db 61 QIMVDDEKQVLTINILQMSWTDHYLQNNVSEYGVKTVRPDGOIKWPDILLYNSADE 120
Qy 121 RFDATFHTNVLVNSSGHCYLPPIKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
Db 121 RFDATFHTNVLVNSSGHCYLPPIKSSCYIDVRWFPDVQHCCLKFGSWSYGGWSLDL 180
Qy 181 QMQEADISGYIPNGEWDLVGIFPKRSERFEYCKEYPDPVTPVTVMRRRTLYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIFPKRSERFEYCKEYPDPVTPVTVMRRRTLYGLNLLIP 240
Qy 241 CVLISALALLVLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTAVILLNWCANFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVVTVIVLQYHHDDPGGKMPKWTAVILLNWCANFLRMKRPGEKVRPACQHK 360
Qy 361 QRCRSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Db 361 QRCRSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVTPDPSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRCDSEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 10
ADE57310
ID ADE57310 standard; protein; 502 AA.
XX ADE57310;
XX 29-JAN-2004 (first entry)
XX Human Protein P36544, SEQ ID NO 3171.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX WO2003016475-A2.
PN

XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEMO) GEN HOSPITAL CORP.
XX PA (FARK) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; P36544.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a human protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 502 AA;
Query Match 100.0%; Score 2702; DB 7; Length 502;
Best Local Similarity 100.0%; Pred. No. 6.9e-264;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRCSPGGVMLAASLLHVSQGEFQKLYKELVKYNFLERPVANDSQPLTVFSLSL 60
DB 1 MRCSPGGVMLAASLLHVSQGEFQKLYKELVKYNFLERPVANDSQPLTVFSLSL 60
QY 61 QIMDVDEKQVLTNTLWQSWTDHVLQNVSEYPGVKTVPDQGIWKPDIILLYNSADE 120
DB 61 QIMDVDEKQVLTNTLWQSWTDHVLQNVSEYPGVKTVPDQGIWKPDIILLYNSADE 120
QY 121 RFDATHTNVLNNSGHCQVLPFGIKSCYIDVRWFFPDVQCKLFGSWSYCGNSLDL 180
DB 121 RFDATHTNVLNNSGHCQVLPFGIKSCYIDVRWFFPDVQCKLFGSWSYCGNSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGPKGRSERFYECCKEPYDVTFTVTRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGPKGRSERFYECCKEPYDVTFTVTRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFAST 300

DB 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIIVGLSVVTVIVLOYHHDPDGGKMPKWTREVILLNWCAMFLMKRPGEDKVRPACQHK 360
DB 301 MIIIVGLSVVTVIVLOYHHDPDGGKMPKWTREVILLNWCAMFLMKRPGEDKVRPACQHK 360
QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTDPDSGVVCGMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTDPDSGVVCGMACSPTHDEHL 420
QY 421 LHGGQPPGEGDPLAKILEEVYIANRFRQDESEAVCSEWKFAPACVDRLCIMAFSVFTI 480
DB 421 LHGGQPPGEGDPLAKILEEVYIANRFRQDESEAVCSEWKFAPACVDRLCIMAFSVFTI 480
QY 481 ICTIGILMSAFNFVEAVSKDFA 502
DB 481 ICTIGILMSAFNFVEAVSKDFA 502
RESULT 11
AAW69216
ID AAW69216 standard; protein; 502 AA.
AC AAW69216;
XX 09-OCT-1998 (first entry)
DT V274T variant human alpha7 nAChR protein.
DE Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer;
KW neurodegeneration; enzyme dysfunction; affective disorder; therapy;
KW immune dysfunction; diabetic neuropathy; Alzheimer's disease;
KW schizophrenia.
XX Homo sapiens.
XX WO9828331-A2.
XX 02-JUL-1998.
XX 22-DEC-1997; 97WO-US023405.
XX 20-DEC-1996; 96US-00771737.
XX (ABBO) ABBOTT LAB.
XX Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM, Roch J;
XX Sullivan JP, Touma E;
XX WPI; 1998-377593/32.
XX N-PSDB; AAV44687.
XX Nucleic acid encoding variant of human alpha 7 nicotinic acetylcholine
XX receptor sub-unit - used to identify modulators of the receptor,
XX potentially useful for treating neuro-degeneration, cancer etc.
XX Claim 15; Fig 2; 44pp; English.
XX This sequence is the V247T variant of human alpha7 nicotinic
XX acetylcholine receptor (nAChR) subunit of the invention. Cells containing
XX the DNA are used to express the protein and to identify modulators of
XX alpha7 nAChR activity or cytoprotective agents, e.g. antisense compounds
XX or antagonists that are potentially useful for treating
XX neurodegeneration, enzyme dysfunction, affective disorders and immune
XX dysfunction, such as cancer, post-herpetic neuralgia, diabetic
XX neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
XX psychosis and schizophrenia. Probes based on the DNA are used to detect
XX the DNA in usual hybridisation or amplification tests, while monoclonal
XX antibodies are used to detect the protein for diagnosis (in vitro or by
XX in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,
XX the protein has about 100-fold greater sensitivity to cholinergic
XX receptor agonists (nicotine or acetylcholine) and response to these

CC agonists decays more slowly, but the wild-type inward rectification is retained

XX Sequence 502 AA;

XX Query Match 99.9%; Score 2698; DB 2; Length 502;

XX Best Local Similarity 99.8%; Pred. No. 1.7e-263;

XX Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60

DB 1 MRCSPGGVWLAALASLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60

QY 61 QIMDVDEKNQVLTNIWQMSWTDHYLQMNVSYPGVKTVRFDPGQIWKPDILLYNSADE 120

DB 61 QIMDVDEKNQVLTNIWQMSWTDHYLQMNVSYPGVKTVRFDPGQIWKPDILLYNSADE 120

QY 121 RFDAFTHTNVLNVSNGHCQVLPFGIFKSSCYIDVRFPFDVQHCKLFGWSYCGNSLDL 180

DB 121 RFDAFTHTNVLNVSNGHCQVLPFGIFKSSCYIDVRFPFDVQHCKLFGWSYCGNSLDL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVTMRRRTLYYGLNLLIP 240

DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVTMRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLLPADSGEKISLGIITVLLSLTVFLLVAEIMPATSDSVPLIAQYFAS 300

DB 241 CVLISALALLVFLLPADSGEKISLGIITVLLSLTVFLLVAEIMPATSDSVPLIAQYFAS 300

QY 301 MIIVGLSVVTVIVLYQHHDPPDGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHK 360

DB 301 MIIVGLSVVTVIVLYQHHDPPDGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHK 360

QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCYPTPDSGVVCGMACSPTHDEHL 420

DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCYPTPDSGVVCGMACSPTHDEHL 420

QY 421 LHGGOPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480

DB 421 LHGGOPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480

QY 481 ICTGILMSAPNFVEAVSKDFA 502

DB 481 ICTGILMSAPNFVEAVSKDFA 502

RESULT 12

AAB50015

ID AAB50015 standard; protein; 502 AA.

AC AAB50015;

XX AAB50015;

XX 14-MAR-2001 (first entry)

XX Mutant human alpha7 ligand gated ion channel #1.

XX Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;

KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 230 /note= "Wild-type Thr substituted by Pro"

XX WO200073431-A2.

XX 07-DEC-2000.

XX 25-MAY-2000; 2000WO-US011862.

XX 27-MAY-1999; 99US-0136174P.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Groppi VB, Wolfe ML, Berkenpas MB;

XX WPI; 2001-061524/07.

XX N-PSDB; AAC90385.

XX Special cell culture medium for treating cells and for inducing mammalian cell lines to conduct calcium ions, comprising specified concentrations of ions of sodium, calcium and potassium at specified pH.

XX Claim 100; Page 70-72; 77pp; English.

XX The present sequence is a mutant human alpha7 nicotinic acetylcholine gated ion channel. The human alpha7 ion channel was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells in the present invention, resulting in preferential calcium ion conductance by the cells

XX Sequence 502 AA;

XX Query Match 99.8%; Score 2696; DB 4; Length 502;

XX Best Local Similarity 99.8%; Pred. No. 2.8e-263;

XX Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60

DB 1 MRCSPGGVWLAALASLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSL 60

QY 61 QIMDVDEKNQVLTNIWQMSWTDHYLQMNVSYPGVKTVRFDPGQIWKPDILLYNSADE 120

DB 61 QIMDVDEKNQVLTNIWQMSWTDHYLQMNVSYPGVKTVRFDPGQIWKPDILLYNSADE 120

QY 121 RFDAFTHTNVLNVSNGHCQVLPFGIFKSSCYIDVRFPFDVQHCKLFGWSYCGNSLDL 180

DB 121 RFDAFTHTNVLNVSNGHCQVLPFGIFKSSCYIDVRFPFDVQHCKLFGWSYCGNSLDL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVTMRRRTLYYGLNLLIP 240

DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVFTVTMRRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLLPADSGEKISLGIITVLLSLTVFLLVAEIMPATSDSVPLIAQYFAS 300

DB 241 CVLISALALLVFLLPADSGEKISLGIITVLLSLTVFLLVAEIMPATSDSVPLIAQYFAS 300

QY 301 MIIVGLSVVTVIVLYQHHDPPDGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHK 360

DB 301 MIIVGLSVVTVIVLYQHHDPPDGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHK 360

QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCYPTPDSGVVCGMACSPTHDEHL 420

DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCYPTPDSGVVCGMACSPTHDEHL 420

QY 421 LHGGOPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480

DB 421 LHGGOPPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFACVVDRLCLMAFSVFTI 480

QY 481 ICTGILMSAPNFVEAVSKDFA 502

DB 481 ICTGILMSAPNFVEAVSKDFA 502

RESULT 13

AAB50016

ID AAB50016 standard; protein; 502 AA.

XX AAB50016;

XX 14-MAR-2001 (first entry)

XX Mutant human alpha7 ligand gated ion channel #2.

XX Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
XX Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 241 /note= "Wild-type Cys substituted by Ser"
XX WO200073431-A2.
XX 07-DEC-2000.
XX 25-MAY-2000; 2000WO-US011862.
XX 27-MAY-1999; 99US-0136174P.
XX (PHAA) PHARMACIA & UPJOHN CO.
XX Groppi VE, Wolfe ML, Berkenpas MB;
XX WPI; 2001-061524/07.
XX N-PSDB; AAC90386.
XX Special cell culture medium for treating cells and for inducing mammalian
PT cell lines to conduct calcium ions, comprising specified concentrations
PT of ions of sodium, calcium and potassium at specified pH.
XX Claim 102; Page 72-74; 77pp; English.
XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
CC gated ion channel. The human alpha7 ion channel was used in the
CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
CC ion channel can be expressed by recombinant cells in the present
CC invention, resulting in preferential calcium ion conductance by the cells
XX Sequence 502 AA;
SQ
Query Match 99.6%; Score 2692; DB 4; Length 502;
Best Local Similarity 99.8%; Pred. No. 7.1e-263;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAALAAALHVSLSQGEFQKLYKELVKNYNPLERPVANDSPLTVYFSLSL 60
Db 1 MRCSPGGVWLAALAAALHVSLSQGEFQKLYKELVKNYNPLERPVANDSPLTVYFSLSL 60
QY 61 QIMDVEKQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIKWPDILLYNSADE 120
Db 61 QIMDVEKQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIKWPDILLYNSADE 120
QY 121 RPDATHNTNVLNNSGHCQVLPDGI FKSSCYIDVRWPPFDVQCKLKFGSWSGWSL 180
Db 121 RPDATHNTNVLNNSGHCQVLPDGI FKSSCYIDVRWPPFDVQCKLKFGSWSGWSL 180
QY 181 QMGEADISGYPNGEWDLVGIPGRSERFEYCKEYPDVTFTVWRRRLYYGLNLLIP 240
Db 181 QMGEADISGYPNGEWDLVGIPGRSERFEYCKEYPDVTFTVWRRRLYYGLNLLIP 240
QY 241 CVLISALALVFLPADSGEKISLGITVLLSLTVFLLVAEIMPATSDSVPILIAQYFAS 300
Db 241 SVLISALALVFLPADSGEKISLGITVLLSLTVFLLVAEIMPATSDSVPILIAQYFAS 300
QY 301 MIIVGLSVTVTVIVLYQHHDDPDGCKMPKWTTRVILLNWCANFLMKPGEKVRPACQHK 360
Db 301 MIIVGLSVTVTVIVLYQHHDDPDGCKMPKWTTRVILLNWCANFLMKPGEKVRPACQHK 360
QY 361 QRCCLASVMSAVAPPPASNGNLLYIGFRLGDCVHCVPDPDSGVCGMACSPTHDEHL 420
Db 361 QRCCLASVMSAVAPPPASNGNLLYIGFRLGDCVHCVPDPDSGVCGMACSPTHDEHL 420

QY 421 LHGGQPPEGDPDLAKILEEVRYIANRFRCDSEAVCSEWKFACVVDRLCIMAFAVPTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANRFRCDSEAVCSEWKFACVVDRLCIMAFAVPTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
RESULT 14
AAB50017
ID AAB50017 standard; protein; 502 AA.
XX AC AAB50017;
XX 14-MAR-2001 (first entry)
XX Mutant human alpha7 ligand gated ion channel #3.
XX Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
XX Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 230 /note= "Wild-type Thr substituted by Pro"
FT Misc-difference 241 /note= "Wild-type Cys substituted by Ser"
XX WO200073431-A2.
XX 07-DEC-2000.
XX 25-MAY-2000; 2000WO-US011862.
XX 27-MAY-1999; 99US-0136174P.
XX (PHAA) PHARMACIA & UPJOHN CO.
XX Groppi VE, Wolfe ML, Berkenpas MB;
XX WPI; 2001-061524/07.
XX N-PSDB; AAC90387.
XX Special cell culture medium for treating cells and for inducing mammalian
PT cell lines to conduct calcium ions, comprising specified concentrations
PT of ions of sodium, calcium and potassium at specified pH.
XX Claim 104; Page 75-77; 77pp; English.
XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
CC gated ion channel. The human alpha7 ion channel was used in the
CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
CC ion channel can be expressed by recombinant cells in the present
CC invention, resulting in preferential calcium ion conductance by the cells
XX Sequence 502 AA;
SQ
Query Match 99.4%; Score 2686; DB 4; Length 502;
Best Local Similarity 99.6%; Pred. No. 2.9e-262;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAALAAALHVSLSQGEFQKLYKELVKNYNPLERPVANDSPLTVYFSLSL 60
Db 1 MRCSPGGVWLAALAAALHVSLSQGEFQKLYKELVKNYNPLERPVANDSPLTVYFSLSL 60
QY 61 QIMDVEKQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIKWPDILLYNSADE 120
Db 61 QIMDVEKQVLTNTNWLQMSWTDHYLQMNVSYPGVKTVRFPDGGQIKWPDILLYNSADE 120

121 RFDAFTHTNVNNSGHCQVLPFGIFKSSCYIDVRFPDVOHQCKLKFGSWSYGGWSLDL 180
121 RFDAFTHTNVNNSGHCQVLPFGIFKSSCYIDVRFPDVOHQCKLKFGSWSYGGWSLDL 180
181 QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRPLYGLMLLP 240
181 QMQEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRPLYGLMLLP 240
241 CVLISALALVFLPADSGEKISLGTIVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
241 SVLISALALVFLPADSGEKISLGTIVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
301 MIIVGLSVVVTIVLQYHHDDPGGKMPKTRVILLNWCAWFLMRKPGDKVRPACQHK 360
301 MIIVGLSVVVTIVLQYHHDDPGGKMPKTRVILLNWCAWFLMRKPGDKVRPACQHK 360
361 QRCCLASVEMSAVAPPPASGNLLYIGFGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
361 QRCCLASVEMSAVAPPPASGNLLYIGFGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
421 LHGGQPPGPDPLAKILLEVRVYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
421 LHGGQPPGPDPLAKILLEVRVYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
481 ICTIGILMSAPNFVEAVSKDFA 502
481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 15

AD57308
ID ADE57308 standard; protein; 502 AA.

AC ADE57308;

DT 29-JAN-2004 (first entry)

XX Rat Protein Q05941, SEQ ID NO 3169.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; Q05941.

XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 502 AA;

Query Match 93.8%; Score 2535; DB 7; Length 502;

Best Local Similarity 93.8%; Pred. No. 5.4e-247;

Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 6 GGVWLAALASLHVLSLQGEFORLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65

Db 6 GGIWLAALASLHVLSLQGEFORLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65

QY 66 DEKNQVLTINWLMQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDIILLNSADDERDAT 125

Db 66 DEKNQVLTINWLMQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDIILLNSADDERDAT 125

QY 126 FHTNVLNNSGHCQVLPFGIFKSSCYIDVRFPDVOHQCKLKFGSWSYGGWSLDLQMOEA 185

Db 126 FHTNVLNNSGHCQVLPFGIFKSSCYIDVRFPDVOHQCKLKFGSWSYGGWSLDLQMOEA 185

QY 186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRPLYGLMLLPVCLIS 245

Db 186 DISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRPLYGLMLLPVCLIS 245

QY 246 ALALLVFLPADSGEKISLGTIVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 305

Db 246 ALALLVFLPADSGEKISLGTIVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 305

QY 306 LSVVTVTVLQYHHDDPGGKMPKTRVILLNWCAWFLMRKPGDKVRPACQHKPRCS 365

Db 306 LSVVTVTVLQYHHDDPGGKMPKTRVILLNWCAWFLMRKPGDKVRPACQHKPRCS 365

QY 366 LASVEMSAVAPPPASGNLLYIGFGLDGVHCVPTPDGSGVCGRMACSPTHDEHLHGGQ 425

Db 366 LASVEMSAVAPPPASGNLLYIGFGLDGVHCVPTPDGSGVCGRMACSPTHDEHLHGGQ 425

QY 426 PPEGDDPLAKILLEVRVYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTICTIG 485

Db 426 PPEGDDPLAKILLEVRVYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTICTIG 485

QY 486 ILMGAPNFVEAVSKDFA 502

Db 486 ILMGAPNFVEAVSKDFA 502

Search completed: May 5, 2004, 15:30:00
Job time : 52 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 17:59:31 ; Search time 5017 Seconds
(without alignments)

11166.325 Million cell updates/sec

Title: US-09-703-951a-11

Perfect score: 1876

Sequence: 1 GGCGCAGGCGGCGAGCCCGG.....TGCTGTGAAGCCCTTCGGA 1876

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_estc.*

9: gb_est1.*

10: gb_est2.*

11: gb_est3.*

12: gb_est4.*

13: gb_est5.*

14: gb_est6.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	936	49.9	1201	9	AL530299
2	788.4	42.0	1201	9	AL563701
3	784.4	41.8	1034	13	BX386932
4	784	41.8	908	13	BUI49265

5	698.2	37.2	1034	13	BX403124
6	653.6	34.8	731	12	BG395536
7	653.2	34.8	738	12	BG925223
8	603.4	32.2	615	14	CB149460
9	560.4	29.9	1084	13	BQ894356
10	517.4	27.6	817	12	BM451308
11	506.4	27.0	536	12	BI963064
12	491.4	26.2	954	9	AA706348
13	488.4	26.0	490	13	BX282644
14	488	26.0	795	12	BG288825
15	486.8	25.9	1080	13	BQ070018
16	480.8	25.6	784	14	CA325260
17	478.6	25.5	640	14	CB244439
18	458.8	24.5	789	9	AI742004
19	447	23.8	922	13	BU915857
20	443.6	23.6	1125	13	BUI48759
21	420.4	22.4	513	9	AA436529
22	376.8	20.1	651	12	BI917899
23	371.6	19.8	443	9	AV727668
24	362.2	19.3	2296	14	CD013901
25	354.4	18.9	530	9	AA612742
26	350.6	18.7	443	14	W31507
27	332.4	17.7	1259	13	BX350024
28	332.2	17.7	586	13	BX299163
29	331	17.6	480	10	BF507825
30	329.2	17.5	635	13	BU680930
31	323.4	17.2	502	9	AA622550
32	323	17.2	549	9	AA418899
33	306.8	16.4	560	14	W52861
34	306.8	16.4	665	10	BB626178
35	306.8	16.4	2815	11	AK034208
36	305	16.3	613	13	BU619901
37	294.2	15.7	885	12	BG632919
38	289.4	15.4	2940	11	AK034228
39	289.4	15.4	3230	11	AK083157
40	283.4	15.1	1436	29	AY402873
41	280	14.9	1864	11	AK053497
42	280	14.9	2916	11	AK051730
43	280	14.9	3126	11	AK080415
44	278.6	14.9	1436	29	AY402874
45	276.2	14.7	477	9	AI306136

ALIGNMENTS

RESULT 1

AL530299

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL530299 1201 bp mRNA linear EST 23-MAY-2003
AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.

AL530299.2 GI:31068132

EST.

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li W.B., Gruber C., Jesses, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12793792.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

7646.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DD007CH030P1&cluster=7646.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

BX403124 BX403124
BG395536 602458136
BG925223 HNC73-1-B
CB149460 K-EST0205
BQ894356 AGENCOURT
BM451308 AGENCOURT
BI963064 1662C10.Y
AA706348 ah28h12.s
BX282644 BX282644
BG288825 602388156
BQ070018 AGENCOURT
CA325260 UT-M-PYO-
CB244439 UT-M-FYO-
AI742004 wg37f08.x
BU915857 AGENCOURT
BUI48759 AGENCOURT
AA436529 zw01901.r
BI917899 603181651
AV727668 AV727668
CD013901 90134548
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W31507 zb92e05.r1
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AA418899 zw01901.s
W52861 zc03e02.r1
BB626178 BB626178
AK034208 Mus muscu
BU619901 UI-H-PH1-
BG632919 GH16126.3
AK034228 Mus muscu
AK083157 Mus muscu
AY402873 Homo sapi
AK053497 Mus muscu
AK051730 Mus muscu
AK080415 Mus muscu
AY402874 Pan trogl
AI306136 qi04f10.x

Db	721	GG	722	
FEATURES	Location/Qualifiers			
1. .731	/organism="Homo sapiens"			
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	/db_xref="taxon:9606"			
	/clone="IMAGE:4580408"			
	/tissue_type="retinoblastoma"			
	/lab_host="DH10B (phage-resistant)"			
	/clone_lib="NIH_MGC_16"			
	/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."			
ORIGIN				
Query Match	34.8%;	Score	653.6;	DB 12; Length 731;
Best Local Similarity	94.9%;	Pred. No.	2.8e-118;	
Matches	68;	Conservative	1;	Mismatches 35; Indels 1; Gaps 1;
Qy	900	GCTGCTCGTGGCTGAGATCATGCCCGCAACATCCGATTCGGTACCATGATAGCCAGTA	959	
Db	2	GCTGCTCGTGGCTGAGATCATGCCCGCAACATCCGATTCGGTACCATGATAGCCAGTA	61	
Qy	960	CTTGGCCAGCACCATGATCATGTCGGCTCTCGGTGTGTGAGCGGTGATCGTGTGCA	1019	
Db	62	CTTGGCCAGCACCATGATCATGTCGGCTCTCGGTGTGTGAGCGGTGATCGTGTGCA	121	
Qy	1020	GTACCCACACACGACCCCGACGGGGGCAAGATGCCAAGTGGACACGAGTCATCCTTCT	1079	
Db	122	GTACCCACACACGACCCCGACGGGGGCAAGATGCCAAGTGGACACGAGTCATCCTTCT	181	
Qy	1080	GAATGTGTGGCTGTGTTCTTSCAATGAAGAGGCCCGGGAGGACAAAGTGTGCGCCGGC	1139	
Db	182	GAATGTGTGGCTGTGTTCTTSCAATGAAGAGGCCCGGGAGGACAAAGTGTGCGCCGGC	241	
Qy	1140	CTGCACACAAGCAGCGGGCTGCAGCTGGCCAGTGTGGAGATGAGCGCGTGGCGCC	1199	
Db	242	CTGCACACAAGCAGCGGGCTGCAGCTGGCCAGTGTGGAGATGAGCGCGTGGCGCC	301	
Qy	1200	GCGCCCGCAGCAACGGGAACCTGTGTACATCGGCTTCGCGGCTTGGACGGCGTGCA	1259	
Db	302	GCGCCCGCAGCAACGGGAACCTGTGTACATCGGCTTCGCGGCTTGGACGGCGTGCA	361	
Qy	1260	CTGTGTCGCCACCCCGACTCTGGGTAGTGTGCGCGCAGTGTGTCGCCACGCA	1319	
Db	362	CTGTGTCGCCACCCCGACTCTGGGTAGTGTGCGCGCAGTGTGTCGCCACGCA	420	
Qy	1320	CGATGAGCACTCTGTGACGCGCGGCAACCCCGAGGGGGACCCGGAATTGGCCAAAT	1379	
Db	421	CGATGAGCACTCTGTGACGCGCGGCAACCCCGAGGGGGACCCGGAATTGGCCAAAT	480	
Qy	1380	CCTGGAGGGTTCGGCTACATTCGCATCGCTTCGCTGCCAGGAGGAGGCGGT	1439	
Db	481	CCTGGAGGGTTCGGCTACATTCGCATCGCTTCGCTGCCAGGAGGAGGCGGT	540	
Qy	1440	CTGCAGGAGTGGGAAGTTCGCGCGCTGTGTGGTGGACCCGCTGTGCTCATGGCTTCTC	1499	
Db	541	CTGCAGGAGTGGGAAGTTCGCGCGCTGTGTGGTGGACCCGCTGTGCTCATGGCTTCTC	600	
Qy	1500	GGTCTTACCATCATCTTGACCATTCGCGCATCTGATGTGGTCCCACTTCGTGAGGC	1559	
Db	601	GGTCTTACCATCATCTTGACCATTCGCGCATCTGATGTGGTCCCACTTCGTGAGGC	660	
Qy	1560	CGTGTCAAAGACATTTCGTAAACCAACCCCTGTTCTGTATCATGTGGAACACTCACAGATG	1619	
Db	661	CGTGTCAAAGACATTTCGTAAACCAACCCCTGTTCTGTATCATGTGGAACACTCACAGATG	720	
Qy	1620	GG	1621	

QY 1550 TCGTGGAGCCGCTGTCACCAAGCTTTCGTAACCAAGCTGGTTCGTACATGTGGAATA 1609
 DB 425 TCGTGGAGCCGCTGTCACCAAGCTTTCGTAACCAAGCTGGTTCGTACATGTGGAATA 484
 QY 1610 CTCACAGATGGGCAAGCCCTTTGGCTTGGCGAGATTGGGGGTGCTTAATCCAGGACAGCA 1669
 DB 485 CTCACAGATGGGCAAGCCCTTTGGCTTGGCGAGATTGGGGGTGCTTAATCCAGGACAGCA 544
 QY 1670 TTACAGCCCAACCTCAGTGTTCCTTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1729
 DB 545 TTACAGCCCAACCTCAGTGTTCCTTCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 604
 QY 1730 TGTACTTTAGGTAGTATGATCTCAGCACTTTCTTTCATATCTCAGATGGGCTGATAGA 1789
 DB 605 TGTACTTTAGGTAGTATGATCTCAGCACTTTCTTTCATATCTCAGATGGGCTGATAGA 664
 QY 1790 TATCTTTGGCACATCCGTACCATCGTTCAGCAGGGCCATGAGTATGCTTTTGGCCATT 1849
 DB 665 TATCTTTGGCACATCCGTACCATCGTTCAGCAGGGCCATGAGTATGCTTTTGGCCATT 724
 QY 1850 AGCCCACTGCTGG 1863
 DB 725 AGCCCACTGCTGG 738

RESULT 8
 CBI49460
 LOCUS
 DEFINITION K-EST0205995 L15CKK1 Homo sapiens cDNA clone L15CKK1-50-D08 5', mRNA linear EST 29-JAN-2003

ACCESSION CBI49460.1 GI:28132277

VERSION CBI49460

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 615)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 50 row: D column: 08

High quality sequence stop: 615.

Location/Qualifiers

1. .615

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="L15CKK1-50-D08"

/sex="M"

/cell_line="CK-K1"

/lab_host="Top10P"

/clone_lib="L15CKK1"

/note="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;

Site 2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then deacapped

with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including

EcoRI site by treatment of T4 RNA ligase and the first

strand cDNA was synthesized from oligo dT-selected mRNA by

priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10P, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 32.2%; Score 603.4; DB 14; Length 615;
 Best Local Similarity 99.0%; Pred. No. 2e-108;
 Matches 607; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 419 ACAGTCTCATGAGCGCTTTGACGCCACATTCACACATCAACGTTGGTGGATTCCTTCG 478
 DB 3 ATATTCTCATAAACGCTTTGACGCCACATTCACACATCAACGTTGGTGGATTCCTTCG 62
 QY 479 GGCATTGCCAGTACCTCCAGGCATATTAAGAGATTCCCTGCTACATCGATGACGCT 538
 DB 63 GGCATTGCCAGTACCTCCAGGCATATTAAGAGATTCCCTGCTACATCGATGACGCT 122
 QY 539 GGTTCCTCCCTTTGATGTGCGACACTGCAAACTGAAGTTTGGTCTCTGGTCTTACGGAGCT 598
 DB 123 GGTTCCTCCCTTTGATGTGCGACACTGCAAACTGAAGTTTGGTCTCTGGTCTTACGGAGCT 182
 QY 599 GGTTCCTGATCTGCGAGATGCGAGGCGAGATATCAGTGGCTATATCCCAATGGAGAT 658
 DB 183 GGTTCCTGATCTGCGAGATGCGAGGCGAGATATCAGTGGCTATATCCCAATGGAGAT 242
 QY 659 GGCACCTAGTGGCAATCCCGGCAAGGAGTCAAAAGTTTCTATGAGTGTGCAAAAGAGC 718
 DB 243 GGCACCTAGTGGCAATCCCGGCAAGGAGTCAAAAGTTTCTATGAGTGTGCAAAAGAGC 302
 QY 719 CCTACCCCGATGTCACTTCAAGTGAACATGCGCGCAGGACGCTTACTATGGCTCTCA 778
 DB 303 CCTACCCCGATGTCACTTCAAGTGAACATGCGCGCAGGACGCTTACTATGGCTCTCA 362
 QY 779 ACCTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTGGTGTCTCTCTTCTCTG 838
 DB 363 ACCTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTGGTGTCTCTCTTCTCTG 422
 QY 839 CAGATTCGGGGAGAGATTTCCCTGGGGATAACAGTCTTACTCTCTCTTCTCTTCTCTCA 898
 DB 423 CAGATTCGGGGAGAGATTTCCCTGGGGATAACAGTCTTACTCTCTCTTCTCTTCTCTCA 482
 QY 899 TGCTGCTGCTGGTGGATCATGCCCCCAATCCGATTCGGTACCATTTGATGATGCCAGT 958
 DB 483 TGCTGCTGCTGGTGGATCATGCCCCCAATCCGATTCGGTACCATTTGATGATGCCAGT 542
 QY 959 ACTTGGCGAGCACCATGATCATCTGGGGCTCTCGGTGGTGGTGGTGGTGGTGGTGGTGC 1018
 DB 543 ACTTGGCGAGCACCATGATCATCTGGGGCTCTCGGTGGTGGTGGTGGTGGTGGTGGTGC 602
 QY 1019 AGTACCACCAACCA 1031
 DB 603 AGTACCACCAACCA 615

RESULT 9

BO894356

LOCUS

DEFINITION AGENCOURT_8725920 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6338722

5', mRNA sequence.

ACCESSION BO894356

VERSION BO894356.1 GI:22286370

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1084)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Unpublished: Robert Strausberg, Ph.D.

BO894356 1084 bp mRNA linear EST 16-AUG-2002

AGENCOURT_8725920 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6338722

5', mRNA sequence.

ACCESSION BO894356

VERSION BO894356.1 GI:22286370

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1084)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Unpublished: Robert Strausberg, Ph.D.

Qy	1358	GGGACCCGGAC	TGGGCCAAGATCCTCGAGAGAGTCCGCTACATTTGCCAATCGCCTTCGCGT	14117
Db	1	GGGACCCGGACTTTGGCCAAAGATCTCGAGAGAGTCCGCTACATTTGCCAACCGCTTTCGCGT		60
Qy	1418	GCCAGGACGAAAGCGAGCGCGTCTGCAGCGAGTGGAGATTTGCGCGCTGTGTGTGTGGAC	1477	
Db	61	GCCAGGACGAAAGCGAGCGCGTCTGCAGCGAGTGGAGATTTGCGCGCTGTGTGTGTGGAC	120	
Qy	1478	GCTGTGCTCATGGCCCTTCTCGGTCTTCAACCATCATCTGCACCATCGGCATCCTGATGT	1537	
Db	121	GCTGTGCTCATGGCCCTTCTCGGTCTTCAACCATCATCTGCACCATCGGCATCCTGATGT	180	
Qy	1538	CGGCTCCCAACTTCGTGGAGCGCGTGTCCAAAGACTTTGGGTAAACACGCGCTGTTCTGT	1597	
Db	181	CGGCTCCCAACTTCGTGGAGCGCGTGTCCAAAGACTTTGGGTAAACACGCGCTGTTCTGT	240	
Qy	1598	ACATGTGGAAAAC	TCA CAGATGGCCAGAGCCTTTGGCTTGGCGAGATTTGGGGTGCTAA	1657
Db	241	ACATGTGGAAAAC	TCA CAGATGGCCAGAGCCTTTGGCTTGGCGAGATTTGGGGTGCTAA	300
Qy	1658	TCCAGGACAGCATTTACACGCCACAACTCCAGTGTTCCTCTTCTGGCTGTGATCGTGTTCG	1717	

Db 301 TCACGACGACATACAGCCACCACTCCAGTGTCCCTCTCGCTGCTAGTGTGTC 360
 QY 1718 TTACGGTTCTTGTCTTACTTGGTAGTAGTAAGTCTAGCACTTTGTTTCAATATCTCAGA 1777
 Db 361 TTACGGTTCTTGTCTTACTTGGTAGTAGTAAGTCTAGCACTTTGTTTCAATATCTCAGA 420
 QY 1778 TGGGCTGATAGATATCTTGGCACATCCGATACCATCGTTCAGCAGGCGCCACTGAGTAGTC 1837
 Db 421 TGGGCTGATAGATATCTTGGCACATCCGATACCATCGTTCAGCAGGCGCCACTGAGTAGTC 480
 QY 1838 ATTTGGCCATTAGCCCACTGCTCTGAAAGCCCTTCGGA 1876
 Db 481 ATTTGGCCATTAGCCCACTGCTCTGAAAGCCCTTCGGA 519

RESULT 11
 BI963064
 LOCUS
 DEFINITION
 ie62c10.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 cDNA clone IMAGE:5671315 5' similar to SW:ACH7 HUMAN P36544
 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN PRECURSOR.
 [1] ; mRNA sequence.

ACCESSION
 VERSION
 BI963064.1 GI:16337469

KEYWORDS
 EST.

SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 536)
 Melton, D., Brown, J., Kent, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemiehe, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
 Williams, T., Jackson, Y., and Bowers, Y.

TITLE
 JOURNAL
 COMMENT
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138

Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu) This sequence now available from the IMAGE
 consortium, for clone orders contact: info@image.llnl.gov

High quality sequence stop: 429.
 Location/Qualifiers
 1..536

FEATURES
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organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5671315"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="PH10B"
 /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
 Site 2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dT priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 library was prepared. The library DNA was normalized by
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library

plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an EcoT of
 20 single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

ORIGIN

Query Match 27.0%; Score 506.4; DB 12; Length 536;
 Best Local Similarity 99.8%; Pred. No. 2.5e-89;
 Matches 507; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1369 TTGGCCAAAGATCCCTGGAGAGGTCGGCTACATTGCCAATCGCTTCGGTCCGAGGAGAA 1428
 Db 1 TTGGCCAAAGATCCCTGGAGAGGTCGGCTACATTGCCAATCGCTTCGGTCCGAGGAGAA 60
 QY 1429 AGCGAGCGGTCTGCAGCGAGTGGAAAGTTCCGCCCTGTGTGTGGACCCCTGTGCTC 1488
 Db 61 AGCGAGCGGTCTGCAGCGAGTGGAAAGTTCCGCCCTGTGTGTGGACCCCTGTGCTC 120
 QY 1489 ATGGCCCTTCTCGGTCTTCCACCATCATCTGCACCATCGGCATCCTGATGCGGTCCCAAC 1548
 Db 121 ATGGCCCTTCTCGGTCTTCCACCATCATCTGCACCATCGGCATCCTGATGCGGTCCCAAC 180
 QY 1549 TTGGTGGAGCCGTGTCCAAAGACTTTGCGTAACCAAGCCCTGTTCTGTACATGTGAAA 1608
 Db 181 TTGGTGGAGCCGTGTCCAAAGACTTTGCGTAACCAAGCCCTGTTCTGTACATGTGAAA 240
 QY 1609 ACTCAGAGTGGCAAGCCCTTTGGCTTGGCGAGATTGGGGGTGCTAAATCCAGGACAGC 1668
 Db 241 ACTCAGAGTGGCAAGCCCTTTGGCTTGGCGAGATTGGGGGTGCTAAATCCAGGACAGC 300
 QY 1669 ATTACAGCCCAACTCCAGTGTCCCTTTCGGCTGTGCAATGCGTGTGCTTTCAGGTTTCT 1728
 Db 301 ATTACAGCCCAACTCCAGTGTCCCTTTCGGCTGTGCAATGCGTGTGCTTTCAGGTTTCT 360
 QY 1729 TTGTTACTTTAGGTAGTAGAATCTCAGCACTTTGTTTTCATATTTCTCAGATGGGCTGATAG 1788
 Db 361 TTGTTACTTTAGGTAGTAGAATCTCAGCACTTTGTTTTCATATTTCTCAGATGGGCTGATAG 420
 QY 1789 ATATCTTGGCAGATCCGTATCCATCGTTCAGCGGCGCACTGAGTAGTCATTTTGGCCAT 1848
 Db 421 ATATCTTGGCAGATCCGTATCCATCGTTCAGCGGCGCACTGAGTAGTCATTTTGGCCAT 480
 QY 1849 TAGCCCACTGCTCGAAGCCCTTCGGA 1876
 Db 481 TAGCCCACTGCTCGAAGCCCTTCGGA 508

RESULT 12

AA706348/c

LOCUS

DEFINITION

AA706348

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA706348

1

GI:2716266

EST.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 954)

NCI-CGAP

http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

CNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/ILML at: www-bio.lnl.gov/bbrp/image/image.html Insert Length: 1543 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 461. Location/Qualifiers 1. 954 /organism="Homo sapiens" /mol_type="mrna" /db_xref="taxon:9606" /clone="1240199" /tissue_type="parathyroid tumor" /dev_stage="adult" /lab_host="DH10B (ampicillin resistant)" /note="Organ: parathyroid gland; Vector: pRT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5'-GTGTACCATCTGAGTGGGCGCGCCACCAATTTTTTTTTTTTTT TTTTT-3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."	
Db	407 TTTAGGTAGTAGAATCTCAGACATTTTCTTATATCTCAGATGGGTAGATATCCT 348
Qy	1796 TGGCACATCGTACCATCGTTCAGCAGGCGGACATGAGTATGTCATTTGGCCATTAGCCCA 1855
Db	347 TGGCACATCGTACCATCGTTCAGCAGGCGGACATGAGTATGTCATTTGGCCATTAGCCCA 288
Qy	1856 CTGCCTGGAAAGCCCTTCGGA 1876
Db	287 CTGCCTGGAAAGCCCTTCGGA 267
RESULT 13 BX282644 LOCUS DEFINITION IMAGE:5493819, mRNA sequence. ACCESSION BX282644 VERSION BX282644.1 GI:28615317 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (Bases 1 to 490) AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B. TITLE Human Unigeneset - RZPD3 JOURNAL Unpublished (2003) COMMENT Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGp998C0412118. RZPDLIB; I.M.A.G.E. CDNA Clone Collection; Human Unigeneset - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CloneCards/cgi- bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13u, Primer sequence: CGTTGTAAACGACGCCAGT.	
FEATURES Location/Qualifiers 1. 490 /organism="Homo sapiens" /mol_type="mrna" /db_xref="taxon:9606" /clone="IMAGp998C0412118 ; IMAGE:5493819" /tissue_type="retinoblastoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 67" /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."	
ORIGIN	
Query Match 26.0%; Score 488.4; DB 13; Length 490; Best Local Similarity 99.8%; Pred. No. 8.6e-86; Matches 489; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1357 GGGGACCCGACCTTGGCCAGATCTCTGGAGGAGGTCCTACATTCGCCAATCGCTTCGCG 1416
Db	1 GGGGACCCGACCTTGGCCAGATCTCTGGAGGAGGTCCTACATTCGCCAATCGCTTCGCG 60
Qy	1417 TGCCAGACGAAAGCAGGCGGTCCTCAGCGAGTGAAGTTCGCCGCTGTGTGGTGGAC 1476
Db	61 TGCCAGACGAAAGCAGGCGGTCCTCAGCGAGTGAAGTTCGCCGCTGTGTGGTGGAC 120
Qy	1477 CGCTGTGCTCATGGCTTCTCGGCTTTCACCATCATCTGCACCATCGGCATCTCTGATG 1536

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Db      121  CGCCTGTGCTCATGGCCCTTCGGCTTCCACCATCATCTGCACCATCGGCATCCTGATG 180
QY      1537  TCGGCTCCCAACTTCGTGAGGCGCGTCCAAAGACTTTTCGCTAACACACGCTGTTCTG 1596
Db      181  TCGGCTCCCAACTTCGTGAGGCGCGTCCAAAGACTTTTCGCTAACACACGCTGTTCTG 240
QY      1597  TACATGTGAAAACTCACAGATGGGCAAGCCCTTTGGCTTGGCGAGATTGGGGGTGCTA 1656
Db      241  TACATGTGAAAACTCACAGATGGGCAAGCCCTTTGGCTTGGCGAGATTGGGGGTGCTA 300
QY      1657  ATCCAGACAGCATTAACAGCCCAACTCCAGTGTCCCTTCCTGCTGCTGCTGCTGTTG 1716
Db      301  ATCCAGACAGCATTAACAGCCCAACTCCAGTGTCCCTTCCTGCTGCTGCTGCTGTTG 360
QY      1717  CTTACGGTTCTTTGTTACTTTAGTAGTAGTAATCTCAGACATTTGTTTCATATCTCAG 1776
Db      361  CTTACGGTTCTTTGTTACTTTAGTAGTAGTAATCTCAGACATTTGTTTCATATCTCAG 420
QY      1777  ATGGGCTGATAGATATCTTTGGCAGATCCGATACCATCGGTACAGAGGCCACTGAGTAGT 1836
Db      421  ATGGGCTGATAGATATCTTTGGCAGATCCGATACCATCGGTACAGAGGCCACTGAGTAGT 480
QY      1837  CATTTTGGCC 1846
Db      481  CATTTTGGCC 490

RESULT 14
LOCUS   BG288825
DEFINITION BG288825 795 bp mRNA linear EST 21-FEB-2001
          602388156F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4517221 5',
          mRNA sequence.
ACCESSION BG288825
VERSION   BG288825.1 GI:13044052
KEYWORDS EST.
SOURCE    Homo sapiens
          Homo sapiens (human)
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 795)
AUTHORS  NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone Distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LHAM10409 row: o column: 14
          High quality sequence stop: 686.
          Location/Qualifiers
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              /mol_type="mRNA"
              /db_xref="taxon:9606"
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              /tissue_type="transitional cell papilloma, cell line"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH_MGC_93"
              /note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NotI;
              Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
              Average insert size 1.7 kb. Library enriched for
              full-length clones and constructed by Life Technologies.
              Note: this is a NIH_MGC Library."

FEATURES
         source
         1..795
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           /mol_type="mRNA"
           /db_xref="taxon:9606"
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           /note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NotI;
           Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
           Average insert size 1.7 kb. Library enriched for
           full-length clones and constructed by Life Technologies.
           Note: this is a NIH_MGC Library."

ORIGIN
Query Match 26.0%; Score 488; DB 12; Length 795;
Best Local Similarity 100.0%; Pred. No. 1.3e-85;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1389  GGTCCGCTACATTGGCAATTCGCTTCGGCTGCCAGACGAAAGCGAGCGGTCTGCAGCGA 1448
Db      1  GGTCCGCTACATTGGCAATTCGCTTCGGCTGCCAGACGAAAGCGAGCGGTCTGCAGCGA 60
QY      1449  GTGGAAGTTCCGCGCTGTGTGTGACCGCTGCTCATGGCCCTTCGGTCTTTCAC 1508
Db      61  GTGGAAGTTCCGCGCTGTGTGTGACCGCTGCTCATGGCCCTTCGGTCTTTCAC 120
QY      1509  CATCATCTCCACATCCGATCTGATGTGCGCTCCCAACTTCGTGGAGGCCGTGTCCTAA 1568
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LOCUS   BQ070018
DEFINITION BQ070018 1080 bp mRNA linear EST 02-APR-2002
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ACCESSION BQ070018
VERSION   BQ070018.1 GI:19899064
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SOURCE    Homo sapiens (human)
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1080)
AUTHORS  NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone Distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
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cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match	25.9%;	Score 486.8;	DB 13;	Length 1080;
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Job time : 5042 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 20:38:58 ; Search time 836 Seconds
(without alignments)

10165.387 Million cell updates/sec

Title: US-09-703-951A-11

Perfect score: 1876

Sequence: 1 GGCGCAGGCGCAGCGCCG.....TGCTGGAAAGCCCTTCGGA 1876

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1787	95.3	1964	13 US-10-302-172-180
5	1624.4	86.6	1636	16 US-10-434-364-3
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11	596.8	31.8	692	16 US-10-434-364-16
12	512.2	27.3	968	15 US-10-106-698-1367
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14	392	20.9	494	16 US-10-434-364-19

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ALIGNMENTS

RESULT 1

US-09-892-985-7
; Sequence 7, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:

APPLICANT: Elliot, Kathryn J.
Ellis, Steven B.

Harbold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McAuliffe

STREET: 4250 Executive Square, 7th Floor

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/892, 985

FILING DATE: 27-Jun-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/217,345

FILING DATE: 21-DEC-98

APPLICATION NUMBER: US 08/467,574

FILING DATE: 05-JUN-95

APPLICATION NUMBER: US 08/466,589,

FILING DATE: 05-JUN-95

APPLICATION NUMBER: US 08/028,031

FILING DATE: 08-MAR-93

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L


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; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15403, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MP102-019P1R0MNM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
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; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
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; NAME/KEY: CDS
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US-10-352-684A-55

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[illegible]

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; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. US20040053250A1el Arginine-rich Protein-like Nucleic
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803 ICNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
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779 CGGGAGGAAGATTTCCCTGGGATTAACAGTCTTCTCTCTTCTTACCGTCTTCTGCTGCT 838
Qy |||||
906 CGTGGCTGAGATCATCCCGCAACATCCGATTCGGTACCATTAAGTATGATCCAGTCTCC 965
Db |||||
839 CGTGGCTGAGATCATCCCGCAACATCCGATTCGGTACCATTAAGTATGATCCAGTCTCC 898
Qy |||||
966 CAGCACCATGATCATCGTGGGCTCTCGTGTGTGTGAGCGTGTGATCGTGTGAGTACCA 1025
Db |||||
899 CAGCACCATGATCATCGTGGGCTCTCGTGTGTGTGAGCGTGTGATCGTGTGAGTACCA 958
Qy |||||
1026 CACACGAGCCCGAGCGGGGCAAGATGCCAATGAGTACGAGTACCATCTCTTCTGAGCTG 1085
Db |||||
959 CCACACGAGCCCGAGCGGGGCAAGATGCCAATGAGTACGAGTACCATCTCTTCTGAGCTG 1018
Qy |||||
1086 GTGCGGTGTCTCTCGAATGAAGAGCCCGCGGAGGACAAAGTGTGCGCGCTCGGCA 1145
Db |||||
1019 GTGCGGTGTCTCTCGAATGAAGAGCCCGCGGAGGACAAAGTGTGCGCGCTCGGCA 1078
Qy |||||
1146 GCACAGCAGCGGCTGACGCTGCGCAGTGTGGAGATGAGCGCGGTGCGCGCGCGCC 1205
Db |||||
1079 GCACAGCAGCGGCTGACGCTGCGCAGTGTGGAGATGAGCGCGGTGCGCGCGCGCC 1138
Qy |||||
1206 GCGCAGCAAGGAACTGTGTATCATCGCTTCCGCGGCTGAGCGGCTGCACTGTGT 1265
Db |||||
1139 GCGCAGCAAGGAACTGTGTATCATCGCTTCCGCGGCTGAGCGGCTGCACTGTGT 1198
Qy |||||
1266 CCGGACCCCGACTCTGGGCTAGTGTGTGCGCGCATGGCTGTCTCCCGCAGCAGATGA 1325
Db |||||
1199 CCGGACCCCGACTCTGGGCTAGTGTGTGCGCGCATGGCTGTCTCCCGCAGCAGATGA 1258
Qy |||||
1326 GCACCTCTGCAAGCGGCGCAACCCCGGAGGGGAGCCGGAATGCGCAAGATCTCTGGA 1385
Db |||||
1259 GCACCTCTGCAAGCGGCGCAACCCCGGAGGGGAGCCGGAATGCGCAAGATCTCTGGA 1318
Qy |||||
1386 GGAGGTCCGCTACATTCGCAATCGCTTCCGCTGCGAGGAGGAGGAGGCGGTCTGAG 1445
Db |||||
1319 GGAGGTCCGCTACATTCGCAATCGCTTCCGCTGCGAGGAGGAGGAGGCGGTCTGAG 1378
Qy |||||
1446 CGAGTGGAGTTCGCGGCTGTGTGTGAGCGCGCTGTGCTCATGGCTTCTCGGTCTT 1505
Db |||||
1379 CGAGTGGAGTTCGCGGCTGTGTGTGAGCGCGCTGTGCTCATGGCTTCTCGGTCTT 1438
Qy |||||
1506 CACCATCATCTGCAACCATCGGCATCTCTGATGTGCGCTCCCAACTTCTGTGGAGGCGGTGTC 1565

1439 CACCATCATCTGCAACCATCGGCATCTCTGATGTGGCTCCCAACTTCTGTGGAGGCGGTGTC 1498
Qy |||||
1566 CAAAGACTTTTGGTAAACCAAGCGCTGTCTGTATCATGTGGAATACTCAAGATGGGCAAG 1625
Db |||||
1499 CAAAGACTTTTGGTAAACCAAGCGCTGTCTGTATCATGTGGAATACTCAAGATGGGCAAG 1558
Qy |||||
1626 GCCTTTGGTGGGAGATTTGGGGTGTCTAATCCAGGACAGCAATTAACGCAACATC 1685
Db |||||
1559 GCCTTTGGTGGGAGATTTGGGGTGTCTAATCCAGGACAGCAATTAACGCAACATC 1618
Qy |||||
1686 CAGTGTCCCTTCTGGCTGTGCTGCTGCTTACCGTCTTCTTGTCTTCTTGTAGTAGT 1745
Db |||||
1619 CAGTGTCCCTTCTGGCTGTGCTGCTGCTTACCGTCTTCTTGTCTTCTTGTAGTAGT 1678
Qy |||||
1746 AGAATCTCAGCACTTTGTTTCATATTCAGATGGGTGTATATATCTTGGCACATCC 1805
Db |||||
1679 AGAATCTCAGCACTTTGTTTCATATTCAGATGGGTGTATATATCTTGGCACATCC 1738
Qy |||||
1806 GTACCATCGGTGAGGAGGCGCACTGAGTAGTCAATTTGCCATAGCCCACTGCTCGAA 1865
Db |||||
1739 GTACCATCGGTGAGGAGGCGCACTGAGTAGTCAATTTGCCATAGCCCACTGCTCGAA 1798
Qy |||||
1866 AGCCCTTCGGA 1876
Db |||||
1799 AGCCCTTCGGA 1809
Qy |||||

RESULT 5
US-10-434-364-3
; Sequence 3, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: OM-7 AND QT-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-434-364-3

Query Match 86.6%; Score 1624.4; DB 16; Length 1636;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1628; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 19 GGGCGACAGCCGAGAGCTGGAGCGCGCGCTCGCTGCGAGCTCCGGAGCTCAACATGCGC 78
Db 1 GGGCGAGAGCCGAGAGCTGGAGCGCGCGCTCGCTGCGAGCTCCGGAGCTCAACATGCGC 60
Qy 79 TGCTCGCGGAGGCGCTGTGGCTGTGGCGCGCTCGCTGCGAGCTGCTGCAAGTCTCCCTGCAA 138
Db 61 TGCTCGCGGAGGCGCTGTGGCTGTGGCGCGCTCGCTGCGAGCTGCTGCAAGTCTCCCTGCAA 120
Qy 139 GGGGAGTTCAGAGGAGCTTTACAGGAGCTGGTCAAGAACTACAACTCCCTTGGAGAGG 198
Db 121 GGGGAGTTCAGAGGAGCTTTACAGGAGCTGGTCAAGAACTACAACTCCCTTGGAGAGG 180
Qy 199 CCGTGCCCAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAGCTCTCTGCAATC 258
Db 181 CCGTGCCCAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGAGCTCTCTGCAATC 240
Qy 259 ATGAGCTGGATGAGAGAGAACCAAGTTTAAACCAACCAATTTGGTGGTGAATGTCTTGG 318
Db 241 ATGAGCTGGATGAGAGAGAACCAAGTTTAAACCAACCAATTTGGTGGTGAATGTCTTGG 300

QY 319 ACAGATCACTATTATACAGTGAATGTCTCAGAAATATCCAGGGGTGAAGACTGTTTCGTTTC 378
Db |||||
QY 301 ACAGATCACTATTATACAGTGAATGTCTCAGAAATATCCAGGGGTGAAGACTGTTTCGTTTC 360
Db |||||
QY 379 CCAGATGGCCAGATTGGAAACACAGACATTTCTCTATTAACAGTGTCTGATGAGCGGTTT 438
Db |||||
QY 361 CCAGATGGCCAGATTGGAAACACAGACATTTCTCTATTAACAGTGTCTGATGAGCGGTTT 420
Db |||||
QY 439 GAGCCACATTTCCACACTAAGCTGTCTGTAATTTCTTGGGCATTCGAGTACTCTGCT 498
Db |||||
QY 421 GAGCCACATTTCCACACTAAGCTGTCTGTAATTTCTTGGGCATTCGAGTACTCTGCT 480
Db |||||
QY 499 CCAGGCATATTCAAGAGTTCTCTGCTACATCGATGACGTGGTTTCCCTTTTGATGTGAG 558
Db |||||
QY 481 CCAGGCATATTCAAGAGTTCTCTGCTACATCGATGACGTGGTTTCCCTTTTGATGTGAG 540
Db |||||
QY 559 CACTGAAAACTGAAGTTTGGTCTCTGTTCTTACCGAGGCTGGTCTCTGGATCTCAGATG 618
Db |||||
QY 541 CACTGCAAACTGAAGTTTGGTCTCTGTTCTTACCGAGGCTGGTCTCTGGATCTCAGATG 600
Db |||||
QY 619 CAGGAGCAGATATCAGTGGCTATATCCCAATGAGAACTGGGACCTAGTGGGAATCCCC 678
Db |||||
QY 601 CAGGAGCAGATATCAGTGGCTATATCCCAATGAGAACTGGGACCTAGTGGGAATCCCC 660
Db |||||
QY 679 GGCAGAGGAGTGAAGGTTCTATGAGTGTCTGAAAGAGCCCTACCCCGATGTCACTTTC 738
Db |||||
QY 661 GGCAGAGGAGTGAAGGTTCTATGAGTGTCTGAAAGAGCCCTACCCCGATGTCACTTTC 720
Db |||||
QY 739 ACAGTACCATTCGGCCGAGACGCTCTACTATGSCCTCAACCTGCTGATCCCTGTGTG 798
Db |||||
QY 721 ACAGTACCATTCGGCCGAGACGCTCTACTATGSCCTCAACCTGCTGATCCCTGTGTG 780
Db |||||
QY 799 CTCATCTCCGCCCTCGCCCTGCTGTGTCTCTGCTTCTGAGATTCGGGGAGAAAGATT 858
Db |||||
QY 781 CTCATCTCCGCCCTCGCCCTGCTGTGTGTCTCTGCTTCTGAGATTCGGGGAGAAAGATT 840
Db |||||
QY 859 TCCCTGGGGATAACAGTCTTACTCTCTCTTACCGTCTTCATGCTGCTCTGCTGGCTGAGATC 918
Db |||||
QY 841 TCCCTGGGGATAACAGTCTTAACTTCTTCTTACCGTCTTCATGCTGCTCTGCTGGCTGAGATC 900
Db |||||
QY 919 ATGCCCGCAACATCCGATTCGGTACCATGATGAGCCAGTACTTCCGAGCACCATGATC 978
Db |||||
QY 901 ATGCCCGCAACATCCGATTCGGTACCATGATGAGCCAGTACTTCCGAGCACCATGATC 960
Db |||||
QY 979 ATCGTGGCCCTTCGGTGTGTGACGCTGATGCTGCTGAGTACCAACACCAACACCC 1038
Db |||||
QY 961 ATCGTGGCCCTTCGGTGTGTGACGCTGATGCTGCTGAGTACCAACACCAACACCC 1020
Db |||||
QY 1039 GACGGGGCAAGATCCCAAGTGGACCAAGATCATCTCTTCTGAACTGTFGCGCTGGTTC 1098
Db |||||
QY 1021 GACGGGGCAAGATCCCAAGTGGACCAAGATCATCTCTTCTGAACTGTFGCGCTGGTTC 1080
Db |||||
QY 1099 CTSCEAATTCAGAGCCCGGGAGACAGAGTGGCCCGCTGCGCCGCTGCGACACAGCAGCGG 1158
Db |||||
QY 1081 TGTGCAATGAAGAGCCCGGGAGACAGAGTGGCCCGCTGCGCCGCTGCGACCAAGCAGCGG 1140
Db |||||
QY 1159 CGCTGAGCCTGGCCAGTGTGAGATGAGCGCGCTGGCGCCCGCCCGCCGACCAACCGG 1218
Db |||||
QY 1141 CGCTGAGCCTGGCCAGTGTGAGATGAGCGCGCTGGCGCCCGCCCGCCGACCAACCGG 1200
Db |||||
QY 1219 AACCTGCTGTAATCGCTTTCGGCCCTTGGACCGGCTGCACTGTGTTCGGACCCCGGAC 1278
Db |||||
QY 1201 AACCTGCTGTAATCGCTTTCGGCCCTTGGACCGGCTGCACTGTGTTCGGACCCCGGAC 1260
Db |||||
QY 1279 TCTGGGAGTGTGTGGCCGATGGCTGCTCCCCACGACGATGACACCTCTCTGAC 1338
Db |||||
QY 1261 TCTGGGAGTGTGTGGCCGATGGCTGCTCCCCACGACGATGACACCTCTCTGAC 1320
Db |||||
QY 1339 GCGGGCAACCCCGGAGGGGACCCGGACTTGGCCAAAGATCTGGAGGAGGTTCGCTTAC 1398
Db |||||
QY 1321 GGTGGGCAACCCCGGAGGGGACCCGGACTTGGCCAAAGATCTGGAGGAGGTTCGCTTAC 1380
Db |||||

QY 1399 ATTGCCAATCGCTTCGCTGCCAGGAGCAAGAGCGGCTCTGCAGCGAGTGAAGTTC 1458
Db |||||
QY 1381 ATTGCCAACCGCTTCGCTGCCAGGACGAAAGCGGCTCTGCAGCGAGTGAAGTTC 1440
Db |||||
QY 1459 GCCGCTGTGTGTGACCGCTGTGCTCATGGCCCTTCGCTCTTCCACCATCATCTGC 1518
Db |||||
QY 1441 GCCGCTGTGTGTGACCGCTGTGCTCATGGCCCTTCGCTCTTCCACCATCATCTGC 1500
Db |||||
QY 1519 ACCATCGGCATCTCTGATGTCTCGCTCCCAACTTCGTGGAGCGCTGTCCAAAGATTGGG 1578
Db |||||
QY 1501 ACCATCGGCATCTCTGATGTCTCGCTCCCAACTTCGTGGAGCGCTGTCCAAAGATTGGG 1560
Db |||||
QY 1579 TAACCAAGCTGTCTCTGATCATGTGCAAACTTCACAGATGGCGAGCGCTTGGCTTGG 1638
Db |||||
QY 1561 TAACCAAGCTGTCTCTGATCATGTGCAAACTTCACAGATGGCGAGCGCTTGGCTTGG 1620
Db |||||
QY 1639 CGAGATTGGGGTGC 1654
Db |||||
QY 1621 CGAGATTGGGGTGC 1636
Db |||||
RESULT 6
US-09-954-936-1
; Sequence 1, Application US/09954936
; Publication No. US20030073161A1
; GENERAL INFORMATION: Clark A.
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)...(1514)
US-09-954-936-1
Query Match 82.2%; Score 1543; DB 10; Length 1590;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1555; Conservative 1; Mismatches 21; Indels 0; Gaps 0;
QY 72 CATGGCTGTCTGCCGAGGAGGCTGTGCTGGCGTGGCGCGCTCGCTCCGAGTGC 131
Db |||||
QY 8 CATGAGGTGTAGCCCGGAGGAGTGGCTGGCACTGGCAGCATCTCTCTGACGCTGC 67
Db |||||
QY 132 CTTGCAAGCCGAGTTCCAGAGAACTTTTACAAGAGCTGGTCAAGAACTACAATCCCTT 191
Db |||||
QY 68 CTTGCAAGCCGAGTTCCAGAGAACTTTTACAAGAGCTGGTCAAGAACTACAATCCCTT 127
Db |||||
QY 192 GGAGAGGCCCGTGGCCAAATGACTCTGCAACCACTCAACCGTCTACTTCTCCCTGAGCTCT 251
Db |||||
QY 128 GGAGAGGCCCGTGGCCAAATGACTCTGCAACCACTCAACCGTCTACTTCTCCCTGAGCTCT 187
Db |||||
QY 252 GCAGATCATGAGCTGGATGAGAAACCAAGTTTTTAACCAACCAATTTGGCTGCAAT 311
Db |||||
QY 188 GCAGATCATGAGCTGGATGAGAAACCAAGTTTTTAACCAACCAATTTGGCTGCAAT 247
Db |||||
QY 312 GTCTTGGACAGATCACTATTATTACAGTGGAAATGTGTGACAGAAATATCCAGGGGTGAAGACTGT 371
Db |||||

Db 248 GTCTTGACAGATCACTATTATACAGTGGAAATGTGTGCAATATATCCAGGGGTGAAGACTGT 307
Qy 372 TCGTTTCCAGATGGCCAGATTTCGAAACACAGACATTTCTCTATATAACAGTGTCTGATGA 431
Db 308 TCGTTTCCAGATGGCCAGATTTCGAAACACAGACATTTCTCTATATAACAGTGTCTGATGA 367
Qy 432 GCGTTTGAAGCCACATTCACATTAACAGTGTGGTGAATTCCTTGGGCAATGCCAGTA 491
Db 368 GCGTTTGAAGCCACATTCACATTAACAGTGTGGTGAATTCCTTGGGCAATGCCAGTA 427
Qy 492 CTTGCTCCAGGATATTCAGAGTCTCTGCTACATGATGATGATGATGATGATGATGATGATGAT 551
Db 428 CTTGCTCCAGGATATTCAGAGTCTCTGCTACATGATGATGATGATGATGATGATGATGATGAT 487
Qy 552 TGTGAGCACTGCACAACTGAAGTTTGGGTCTCTGCTTACGAGGCTGGTCTCTTGGATCT 611
Db 488 TGTGAGCACTGCACAACTGAAGTTTGGGTCTCTGCTTACGAGGCTGGTCTCTTGGATCT 547
Qy 612 GCAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGGAGAAATGGGACCTAGTGGG 671
Db 548 GCAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGGAGAAATGGGACCTAGTGGG 607
Qy 672 AATCCCGGCAAGAGGAGTGAAGTCTATGAGTGTGCAAGAGCCCTACCCGATGT 731
Db 608 AATCCCGGCAAGAGGAGTGAAGTCTATGAGTGTGCAAGAGCCCTACCCGATGT 667
Qy 732 CACCTTCAAGTACCATGCGCCGAGGACGCTCTACTATGAGTGTGCAAGAGCCCTACCCGATGT 791
Db 668 CACCTTCAAGTACCATGCGCCGAGGACGCTCTACTATGAGTGTGCAAGAGCCCTACCCGATGT 727
Qy 792 CTGTGTGCTATCTCCGCTCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db 728 CTGTGTGCTATCTCCGCTCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
Qy 852 GAAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 911
Db 788 GAAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCTGCTTCTGCTGCTGCTGCTGCTGCTGCT 847
Qy 912 TGAGATCATGCGCGCAACATCGATTGCGTACCATGATGATGATGATGATGATGATGATGATGATGAT 971
Db 848 TGAGATCATGCGCGCAACATCGATTGCGTACCATGATGATGATGATGATGATGATGATGATGATGAT 907
Qy 972 CATGATCATGCGCGCTCTCGTGTGTGAGCGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1031
Db 908 CATGATCATGCGCGCTCTCGTGTGTGAGCGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
Qy 1032 CGACCCCGACGGGGCAAGATGCCCAAGTGGACCAAGATGCTATCTTCTGAACTGGTGGCG 1091
Db 968 CGACCCCGACGGGGCAAGATGCCCAAGTGGACCAAGATGCTATCTTCTGAACTGGTGGCG 1027
Qy 1092 GTGGTTCTSCGATGAAGAGCCCGGGAGAGCAAGGTGGCCCGCGCTGCGCAGCAAA 1151
Db 1028 GTGGTTCTSCGATGAAGAGCCCGGGAGAGCAAGGTGGCCCGCGCTGCGCAGCAAA 1087
Qy 1152 GCAGCGCGCTGCGACCTGCGCAGTGTGAGATGAGCGCGTGGCGCGCGCGCGCGCGCGCGCGCG 1211
Db 1088 GCAGCGCGCTGCGACCTGCGCAGTGTGAGATGAGCGCGTGGCGCGCGCGCGCGCGCGCGCGCG 1147
Qy 1212 CAAAGGGAACCTGCTGTATCATCGGCTTCGCGCGCTGGAAGCGCGTGTGTGTGTGTGTGTGTGTGT 1271
Db 1148 CAAAGGGAACCTGCTGTATCATCGGCTTCGCGCGCTGGAAGCGCGTGTGTGTGTGTGTGTGTGTGT 1207
Qy 1272 CCCCAGCTCTGGGTAGTGTGTGGCGCATGAGCTGTCTCCCGCAGCGATGAGCACT 1331
Db 1208 CCCCAGCTCTGGGTAGTGTGTGGCGCATGAGCTGTCTCCCGCAGCGATGAGCACT 1267
Qy 1332 CTTGACGCGCGGCAACCCCGAGGGGACCCCGAGCTTGGCAAGATCCTGAGGAGGT 1391
Db 1268 CTTGACGCGCGGCAACCCCGAGGGGACCCCGAGCTTGGCAAGATCCTGAGGAGGT 1327
Qy 1392 CCGCTACATTTGCAATTCGCTTCGCTGCGCAGGACGAAAGCGAGGGGCTGTCGAGCGAGTG 1451

Db 1328 CCGTACATTTGCCAACCGCTTCCGCTGCCAGGACGAAAGCGAGCGGCTCTGCGAGGAGTG 1387
Qy 1452 GAAGTTTCGCGCGCTGTGTGTGGACCGCTGTGCTCATGAGCCCTTTCGGTCTTCCACAT 1511
Db 1388 GAAGTTTCGCGCGCTGTGTGTGGACCGCTGTGCTCATGAGCCCTTTCGGTCTTCCACAT 1447
Qy 1512 CATCTGCACCATCGGCTCTGATGTCGGCTCCCACTTCTGTCGAGCGCTGTCCAAAGA 1571
Db 1448 CATCTGCACCATCGGCTCTGATGTCGGCTCCCACTTCTGTCGAGCGCTGTCCAAAGA 1507
Qy 1572 CTTTGGCTAACACCGCTCTGATACATGTGCAAACTCACAGATGGGCAAGGCTTT 1631
Db 1508 CTTTGGCTAACACCGCTCTGATGTCGGCTCCCACTTCTGTCGAGCGCTGTCCAAAGA 1567
Qy 1632 GGCTTGGCGAGATTGG 1648
Db 1568 GGCTTGGCGAGATTGG 1584

RESULT 7
US-10-434-364-23
; Sequence 23, Application US/10434364
; Publication No. US2004009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND QM-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 1571
; TYPE: DNA
; ORGANISM: Macaca mulatta
; US-10-434-364-23

Query Match 79.9%; Score 1498.6; DB 16; Length 1571;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 1525; Conservative 1; Mismatches 45; Indels 0; Gaps 0;

Qy 67 CTCACATGCGCTCTCGCGGAGGCGTCTGGCTGGCTCTGGCTGGCTCTGGCTGGCTCTGGCTGGCT 126
Db 1 CTCACATGCGCTCTCGCGGAGGCGTCTGGCTGGCTCTGGCTGGCTCTGGCTGGCTCTGGCTGGCT 60
Qy 127 GTGTCCCTGCAAGCGAGTTCACAGGAAGCTTTACAGGAGCTGCTCAAGAACTACAAT 186
Db 61 GTGTCCCTGCAAGCGAGTTCACAGGAAGCTTTACAGGAGCTGCTCAAGAACTACAAT 120
Qy 187 CCCTTGGAGAGCGCGCTGGCCAAATGACTCGCAACACTCAACCGCTCTACTTCTCCCTGAGC 246
Db 121 CCCTTGGAGAGCGCGCTGGCCAAATGACTCGCAACCGCTCAACCGCTCTACTTCTCCCTGAGC 180
Qy 247 CTCCTGAGATCATGAGCGTGGATGAGAAACCAAGTTTAAACCAACCAATTTGGCTG 306
Db 181 CTCCTGAGATCATGAGCGTGGATGAGAAACCAAGTTTAAACCAACCAATTTGGCTG 240
Qy 307 CAAATGCTTGGACAGATCACTATTTACAGTGAATGTGTGAGAAATATCCAGGGGTGAAG 366
Db 241 CAAATGCTTGGACAGATCACTATTTACAGTGAATGTGTGAGAAATATCCAGGGGTGAAG 300
Qy 367 ACTGTTCGTTCCTCAGATGGCCAGATTGGAAACCAAGCAATTTCTTCTATAACAGTGT 426
Db 301 ACTGTTCGTTCCTCAGATGGCCAGATTGGAAACCAAGCAATTTCTTCTATAACAGTGT 360
Qy 427 GATGAGCGCTTGGAGCGCACTTCCACATGAGTGTGTGTAATTTCTTCTGGGCAATTC 486
Db 361 GATGAGCGCTTGGAGCGCACTTCCACCAACGCTGTGTGTAATTTCTTCTGGGCAATTC 420

QY 487 CAGTACCTGCTCCAGGCATATTCAGAGTTCCTGCTACATCGATGTAACGCTGGTTCC 546
Db |||||
QY 421 CAGTACCTGCTCCAGGCATATTCAGAGTTCCTGCTACATCGATGTAACGCTGGTTCC 480
Db |||||
QY 547 TTGATGTGAGCACTGCAAACTGAAGTTTGGTCTCTTACGAGGCTGGTCTCTTG 606
Db |||||
QY 481 TTGATGTGAGCACTGCAAACTGAAGTTTGGTCTCTTACGAGGCTGGTCTCTTG 540
Db |||||
QY 607 GATCTGCAGATGTCAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGACCTA 666
Db |||||
QY 541 GATCTGCAGATGTCAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGACCTA 600
Db |||||
QY 667 GTGGAAATCCCGGCAAGAGGAGTGAAGTTTATAGTGTCTGCTCAAAAGAGCCCTACCC 726
Db |||||
QY 601 GTGGAAATCCCGGCAAGAGGAGTGAAGTTTATAGTGTCTGCTCAAAAGAGCCCTACCC 660
Db |||||
QY 727 GATGTCACTTTCACAGTCAACATCGCGCAGGAGCTCTACTATGGCTCAACCTGCTG 786
Db |||||
QY 661 GATGTCACTTTCACAGTCAACATCGCGCAGGAGCCCTCTACTAGGCTCAACCTGCTG 720
Db |||||
QY 787 ATCCCTGTGTGCTCATCTCGCCCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846
Db |||||
QY 721 ATCCCTGTGTGCTCATCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db |||||
QY 847 GGGGAGAAATTCCTCGGGGATAACAGTCTTACTCTCTTACCGTCTCTATGCTGCTC 906
Db |||||
QY 781 GGGGAGAAATTCCTCGGGGATAACAGTCTTACTCTCTCTCACTGTCTCTCATGCTGCT 840
Db |||||
QY 907 GTGGCTGAGATCATCGCGCAACATTCOGATTCGGTACCATTCATAGCCGAGTCTGCC 966
Db |||||
QY 841 GTGGCTGAGATCATCGCGCAACATTCOGATTCGGTACCATTCATAGCCGAGTCTGCC 900
Db |||||
QY 967 AGCACCATGATCATCTGCGGCTCTCGGTGGTGTGAGCGTATCGTGTGCTGAGTACAC 1026
Db |||||
QY 901 AGCACCATGATCATCTGCGGCTCTCGGTGGTGTGAGCGTATCGTGTGCTGAGTACAC 960
Db |||||
QY 1027 CACACGACCCCGAGCGGGGCAAGATGCCCAGTGGACAGAGTCAATCTTCTGAACTGG 1086
Db |||||
QY 961 CACACGACCCCGAGCGGGGCAAGATGCCCAGTGGACAGAGTCAATCTTCTGAACTGG 1020
Db |||||
QY 1087 TGCGGTGTTCTCGATGAAGAGCCCGGGAGGACAGGTGCGCCGCGCTGCCAG 1146
Db |||||
QY 1021 TGCGGTGTTCTCGATGAAGAGCCCGGGAGGATAGGTGCGCCGCGCTGCCAG 1080
Db |||||
QY 1147 CACACGACCCCGAGCGGCTGAGCGCTGAGTGGAGTGGAGCGCGTGGCGCGCGGCC 1206
Db |||||
QY 1081 CACACGACCCCGAGCGGCTGAGCGCTGAGTGGAGTGGAGCGCGTGGCGCGCGGCC 1140
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QY 1207 GCCAGCAACGGAAACCTGCTGTATATCGGCTTCCGCGGCTGGACGGGATGCAATTCGCG 1266
Db |||||
QY 1141 GCCAGCAACGGAAACCTGCTGTATATCGGCTTCCGCGGCTGGACGGGATGCAATTCGCG 1200
Db |||||
QY 1267 CCGACCCCGAGCTGCGGTGAGTGTGCGCGCTGCTGCGCGCTGCTGCGCGCGCGCTGAG 1326
Db |||||
QY 1201 CCGACCCCGAGCTGCGGTGAGTGTGCGCGCGCTGCTGCGCGCTGCTGCGCGCGCGCTGAG 1260
Db |||||
QY 1327 CACCTCTGACGCGCGGCAACCCCGCGAGGGGAGCCCGGAGTGTGCGCAAGATCTCTGGAG 1386
Db |||||
QY 1261 CACCTCTGACGCGGTGAGTGTGCGCGCGCTGCTGCGCGCTGCTGCGCGCGCGCTGAG 1320
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QY 1387 GAGGTCCGTATCATTCGCTTCCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 1446
Db |||||
QY 1321 GAGGTCCGTATCATTCGCTTCCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 1380
Db |||||
QY 1447 GAGTGAAGTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1506
Db |||||
QY 1381 GAGTGAAGTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Db |||||
QY 1507 ACCATCATCTGACCATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1566
Db |||||
QY 1441 ACCATCATCTGACCATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db |||||
QY 1567 AAAGACTTTGGTAAACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1626
Db |||||

Db 1501 AAAGACTTTGGTAAACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1627 CCTTTGGCTTG 1637
Db 1561 CCTTTGGCTTG 1571
RESULT 8
US-10-434-364-26
; Sequence 26, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND QM-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; TITLE OF INVENTION: THE TRANSFECTED CELLS
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1571
; TYPE: DNA
; ORGANISM: Macaca mulatta
US-10-434-364-26
Query Match 79.6%; Score 1493.8; DB 16; Length 1571;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 48; Indels 0; Gaps 0;
QY 67 CTCACATGCGCTGCTCGCGCGGAGGCGCTCTGGCTGGCGCTGGCGCGCTGCTGCTGCTG 126
Db 1 CTCACATGCGCTGCTCGCGCGGAGGCGCTCTGGCTGGCGCTGGCGCGCTGCTGCTGCTG 60
QY 127 GTGTCCCTGCAAGGCGAGTTCAGAGGAAGCTTTCAAGAGAGCTGGTCAAGAACTACAAAT 186
Db 61 GTGTCCCTGCAAGGCGAGTTCAGAGGAAGCTTTCAAGAGAGCTGGTCAAGAACTACAAAC 120
QY 187 CCCTTGGAGAGCGCGCTGCGCAACATTCGCAACACCTACCGCTCTACTCTCTCCCTGAGC 246
Db 121 CCCTTGGAGAGCGCGCTGCGCAACATTCGCAACACCTACCGCTCTACTCTCTCCCTGAGC 180
QY 247 CTCCTGCGAGATCATCGAGCGTGGATGAGAGAAACCAAGTTTAAACCAACCAATTTGGCTG 306
Db 181 CTCCTGCGAGATCATCGAGCGTGGATGAGAGAAACCAAGTTTAAACCAACCAATTTGGCTG 240
QY 307 CAAATGTCTTGGACAGATCACTATTTACAGTGGAAATGTGTGAGAAATATCCAGGGGTGAG 366
Db 241 CAAATGTCTTGGACAGATCACTATTTACAGTGGAAATGTGTGAGAAATATCCAGGGGTGAG 300
QY 367 ACTGTTCTGTTCCCGAGATGGCCAGATTTGGAAACACAGACATTTCTTCTATACAGTGTCT 426
Db 301 ACTGTTCTGTTCCCGAGATGGCCAGATTTGGAAACACAGACATTTCTTCTATACAGTGTCT 360
QY 427 GATGAGCGCTTTGAGCGCCACATTCACACATCAAGTGTGGTGAATTTCTTCTGGGCAATTC 486
Db 361 GATGAGCGCTTTGAGCGCCACATTCACACATCAAGTGTGGTGAATTTCTTCTGGGCAATTC 420
QY 487 CAGTACCTGCTCCAGGCATATTCAGAGTTCCTGCTACATCGATGTAGCTGGTTTCCC 546
Db 421 CAGTACCTGCTCCAGGCATATTCAGAGTTCCTGCTACATCGATGTAGCTGGTTTCCC 480
QY 547 TTTGATGTGACACTGCGAACTGAGTTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
Db 481 TTTGATGTGACACTGCGAACTGAGTTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 607 GATCTGCAGATGTCAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGGACCTA 666
Db 541 GATCTGCAGATGTCAGGAGGAGATATCAGTGGCTATATCCCAATGGAGATGGGACCTA 600

667 GTGGGATCCCGGCAAGAGGAGTGAAGGTTCTATGAGTGTGCAAGAGCGCTACCC 726
Db GTGGGAATCCCGCAAGAGGAGTGAAGGTTCTATGAGTGTGCAAGAGCGCTACCC 660
QY GATGTCACCTTACAGTGAACCATGCGCGGAGAGCGCTTACTATGCGCTCAACCTGCTG 786
Db GATGTCACCTTACAGTGAACCATGCGCGGAGAGCGCTTACTACGCGCTCAACCTGCTG 720
QY ATCCCTGTGTCTATCTCCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846
Db ATCCCTGTGTCTATCTCCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY GGGGAGAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCGTCTTCACTGCTGCTC 906
Db GGGGAGAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCTTCTCTCTCTCTCTCTCT 840
QY GTGGCTGAGATCATGCGCGCAACATCCGATTCGGTACCAATGATAGCCCAAGTCTTGGCC 966
Db GTGGCTGAGATCATGCGCGCAACATCCGATTCAGTACCAATGATAGCCCAAGTCTTGGCC 900
QY AGCACATGATCATGCTGGGCTCTCGTGGTGTGACGCTGATCGTGTGCTGCTGCTGCTGCT 1026
Db AGCACATGATCATGCTGGGCTCTCGTGGTGTGACGCTGATCGTGTGCTGCTGCTGCTGCT 960
QY CACACGACCCCGAGCGGGGCAAGATGCCCAAGTGAACAGAGTCACTCTTCTGAACTGG 1086
Db CACACGACCCCGAGCGGGGCAAGATGCCCAAGTGAACAGAGTCACTCTTCTGAACTGG 1020
QY TGGCGTGTCTTCCGAAATGAAGAGCGCGGGGAGGACAGAGTGTGCGCGCTGCTGCTGCTG 1146
Db TGGCGTGTCTTCCGAAATGAAGAGCGCGGGGAGGACAGAGTGTGCGCGCTGCTGCTGCTG 1080
QY CACAGCAGCGCGCTGACCTGGCGAGTGTGAGATGAGCGCGCTGCGCGCGCGCGCGCG 1206
Db CACAGCAGCGCGCTGACCTGGCGAGTGTGAGATGAGCGCGCTGCGCGCGCGCGCGCG 1140
QY GCCAGCAACGGGAACCTGTCTGATCATCGGCTTCCGCGCGCTGAGAGCGCGCTGCTGCTG 1266
Db GCCAGCAACGGGAACCTGTCTGATCATCGGCTTCCGCGCGCTGAGAGCGCGCTGCTGCTG 1200
QY CCGACCCCGGACTGTGGGTGAGTGTGGCGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTG 1326
Db CCGACCCCGGACTGTGGGTGAGTGTGGCGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY CACTCTGTCAGCGCGGCAACCCCGAGGGGACCGGACTTGGCCCAAGATCCTGGAG 1386
Db CACTCTGTCACGCTGGGACG 1320
QY GAGTCCGCTACATTTGCCAATCGCTTCCGCTGCCAGGACGAAAGCGAGCGGCTGCGAGC 1446
Db GAGTCCGCTACATTTGCCAATCGCTTCCGCTGCCAGGACGAAAGCGAGCGGCTGCGAGC 1380
QY GAGTGAAGTTCGCGCGCTGTGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506
Db GAGTGAAGTTCGCGCGCTGTGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY ACCATCATCGACCATCGGATCCTGATGTCGGCTGCCAATCTCGTGGAGCGCGCTGCTG 1566
Db ACCATCATCGACCATCGGATCCTGATGTCGGCTGCCAATCTCGTGGAGCGCGCTGCTG 1500
QY AAAGATTTCGCTAACCGCGCTGTGTGATGTCGATGTCGATGTCGATGTCGATGTCGATG 1626
Db AAAGATTTCGCTAACCGCGCTGTGTGATGTCGATGTCGATGTCGATGTCGATGTCGATG 1560
QY CCTTTGGCTTG 1637
Db CCTTGGCTTG 1571

RESULT 9

US-10-434-364-9

; Sequence 9, Application US/10434364

Publication No. US20040009554A1
GENERAL INFORMATION:
APPLICANT: WANG, DAGUANG
TITLE OF INVENTION: QM-7 AND QT-6 CELLS TRANSFECTED WITH MUTANT CELL
TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
TITLE OF INVENTION: THE TRANSFECTED CELLS
FILE REFERENCE: MEMORY-11
CURRENT APPLICATION NUMBER: US/10/434,364
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: 60/378,642
PRIOR FILING DATE: 2002-05-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 1571
TYPE: DNA
ORGANISM: Rattus sp.
US-10-434-364-9

Query Match 64.0%; Score 1200.6; DB 16; Length 1571;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 1317; Conservative 1; Mismatches 195; Indels 0; Gaps 0;

QY 69 CAACATGCGCTGCTCGCGGAGGCGCTCTGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCT 128
Db 2 CACCATGTGCGGCGGCGGAGGAGGATCTGGCTGGCTCTGGCTGGCTCTGGCTGGCTCTGGCTGG 61
QY 129 GTCCTCTGCAAGGCGAGTTCACAGAGAGGCTTTTCAAGGAGGCTGGTCAAGAACTACAAATCC 188
Db 62 GTCCTCTGCAAGGCGAGTTCACAGAGAGGCTTTTCAAGGAGGCTGGTCAAGAACTACAAATCC 121
QY 189 CTTGGAGAGCGCGCTGGCGCAATGACTGCAACCACTACCGCTCTACTCTCTCTCTCTCTCTCT 248
Db 122 GCTGGAGAGCGCGCTGGCGCAATGACTGCAACCACTACCGCTCTACTCTCTCTCTCTCTCTCT 181
QY 249 CTTGGAGAGCGCGCTGGCGCAATGACTGCAACCACTACCGCTCTACTCTCTCTCTCTCTCTCT 308
Db 182 CTTGGAGAGCGCGCTGGCGCAATGACTGCAACCACTACCGCTCTACTCTCTCTCTCTCTCTCT 241
QY 309 AATGCTCTTGACAGATCAGCTATTTTACAGTGGAAATGTGTAGAAATATCCAGGGGTGAAGAC 368
Db 242 AATGCTCTTGACAGATCAGCTATTTTACAGTGGAAATGTGTAGAAATATCCAGGGGTGAAGAA 301
QY 369 TGTTCGTTTCCAGATGCGCGAGATTTTGGAAACAGACATTTCTCTCTATTAACAGTGTCTGA 428
Db 302 TGTTCGTTTCCAGATGCGCGAGATTTTGGAAACAGACATTTCTCTCTATTAACAGTGTCTGA 361
QY 429 TGAGCGCTTTGACGCCACATTTCCACACTAAGCTGTTGGTGAATTTCTCTGGGCAATGCCA 488
Db 362 TGAGCGCTTTGATGCCACATTTCCACACTAAGCTGTTGGTGAATTTCTCTGGGCAATGCCA 421
QY 489 GTACCTGCTTCCAGGCGATATTTCAAGAGTTCCTGCTACATCGATGATGATGATGATGATGAT 548
Db 422 GTATCTCTTCCAGGCGATATTTCAAGAGTTCCTGCTACATTTGACGTTTCGCTGCTGCTGCTGCT 481
QY 549 TGATGTCAGCACTGCAAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 608
Db 482 TGATGTCAGCACTGCAAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 541
QY 609 TCTGCAGATGCAAGGAGGAGATATCAGTGGCTATATCCCAATGGAAGATGGAGGAGGAGGAG 668
Db 542 CTTGCAATGCAAGGAGGAGATATCAGTGGCTATATCCCAATGGAAGATGGAGGAGGAGGAG 601
QY 669 GGGAAATCCCGGCAAGAGGAGTGAAGGTTCTATGATGCTGCAAGAGGAGGAGGAGGAGGAGGAG 728
Db 602 GGGAAATCCCGGCAAGAGGAGTGAAGGTTCTATGATGCTGCAAGAGGAGGAGGAGGAGGAGGAG 661
QY 729 TGTCACTTCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 788
Db 662 TGTCACTTCAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 721
QY 789 CCCCTGTGTCTATCTCCGCGCTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGG 848

Db 722 CCCTTGTTGTACTCATTTTCAGCCCTGGCTCTGCTGCTATTTCTTGCTGCTGCAGACTCTGG 781
Qy 849 GGAGAGATTTCCCTGGGGATAACAGTCTTACTCTCTTACCTGCTCTCATGCTGCTCGT 908
Db 782 AGAGAAAATCTCTTGGAAATACATGCTTAACTTCTCTGACTGCTCTTCTGCTGCTGCT 841
Qy 909 GGCTGAGATCATGCCCGCAACATCCGATTCGGTACCATTTGATAGCCCAAGTACTTTCGCCAG 968
Db 842 GGCTGAGATCATGCCAGCAACATCTGATTTCTGCTTCTGATAGCACAATACTTTCGCCAG 901
Qy 969 CACCATGATCATGCTGGGCTCTCGTGGTGGTGAACGCTGATGCTGCTGCTGCTGCTGCTGCT 1028
Db 902 CACCATGATCATGCTGGGCTCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
Qy 1029 CCAGACCCCGAGCGGGCAGATGCCCAAGTGGACAGAGTCACTCTTCTGAACTGCTG 1088
Db 962 CCATGACCTGATGCTGGCAAAATGCCCTAAGTGGACAGATCACTCTCTGAACTGCTG 1021
Qy 1089 CGCTGGTTCCTSCGAATGAAGAGCCCGGGAGGACAAAGTGGCTGCTGCTGCTGCTGCTGCT 1148
Db 1022 TGCTATGTTTCTGCGCATGAAGAGSCCGGAGAGGACAAAGTGGCTGCTGCTGCTGCTGCT 1081
Qy 1149 CAGCAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1208
Db 1082 CAAAGCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1141
Qy 1209 CAGCAACGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1268
Db 1142 CAGCAATGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1201
Qy 1269 GACCCCGCACTCGGGTGTGTGTGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1328
Db 1202 AACTCCAGACTCTGGGCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1261
Qy 1329 CTTCTGCT 1388
Db 1262 CTTCTGCT 1321
Qy 1389 GGTCCGCTACATTTGCAATCGCTTCCGCTGCCAGGACGAAAGCGGCGGTCTGCAAGCA 1448
Db 1322 GGTCCGCTACATTCGCAACCGCTTCCGCTGCCAGGACGAAAGCGGCGGTCTGCAAGCA 1381
Qy 1449 GTGAAGTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1508
Db 1382 ATGAAGTTTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1441
Qy 1509 CATCATCTGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1568
Db 1442 CATCATCTGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501
Qy 1569 AGACTTTGGGTAA 1581
Db 1502 AGACTTTGGTTAA 1514

RESULT 10
US-10-434-364-15
; Sequence 15, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND QT-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 880

; TYPE: DNA
; ORGANISM: Macaca mulatta
US-10-434-364-15
Query Match 33.9%; Score 635.2; DB 16; Length 880;
Best Local Similarity 93.9%; Pred. No. 1.2e-181;
Matches 672; Conservative 0; Mismatches 43; Indels 1; Gaps 1;
Qy 1161 CTGCAGCTGCTGCCAGTGTGGAGATGAGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1220
Db 1 CTGCAGCTGCTGCCAGTGTGGAGATGAGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Qy 1221 CCTGCTGATCATCGGCTTCCGCGCTGGAGCGGCGTGGAGTGTGTCCGCGCGCGCGCGCGCGCTC 1280
Db 61 CCTGCTGATCATCGGCTTCCGCGCTGGAGCGGCGTGGAGTGTGTCCGCGCGCGCGCGCGCGCTC 120
Qy 1281 TGGGGTAGTGTGGCGCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1340
Db 121 CGGGGTGTGTGGCGCGCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Qy 1341 CGGGCAACCCCGCGAGGGGAGCCCGGACTTGGCCCAAGATCCTGGAGGAGTCCCGTACAT 1400
Db 181 TGGGCGAGCCCGCGAGGGGAGCCCGGACTTGGCCCAAGATCCTGGAGGAGTCCCGTACAT 240
Qy 1401 TGCCAACTGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1460
Db 241 CGCCAAACCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Qy 1461 CGCCTGCT 1520
Db 301 CGCCTGCT 360
Qy 1521 CATCGGCACTCTGATGTGGCTTCCCAACTTGGTGAGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCT 1580
Db 361 CATCGGCACTCTGATGTGGCTTCCCAACTTGGTGAGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy 1581 ACCAGCGCTGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1640
Db 421 ACCAGCGCTGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 1641 AGATTTGGGGTGTAAATCCAGGACAGATTAACGCAACTCCAGTGTTCCTTCTG 1700
Db 481 AGATTTGGGGTGTAAATCCAGGACAGATTAACGCAACTCCAGTGTTCCTTCTG 540
Qy 1701 GCTGTGAGTGTGTGCTTACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1760
Db 541 GCTGTGAGTGTGTGCTTACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 1761 TGTTCATATTTCTGAGTGGCTGATGATATCTTGGCAGATCCGTCACATCCGTCAGCTGCTGCTGCT 1820
Db 601 AGTTTAATACGCTGAGTGGGCTGAT-GATCCCTTGGCAGATCCGTCAGCTGCTGCTGCTGCTGCT 659
Qy 1821 AGGGCCACTGAGTGTGCTATTTTGGCCATTTAGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1876
Db 660 AGGGCCACTGAGTGTGCTATTTTGGCCATTTAGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 715

RESULT 11
US-10-434-364-16
; Sequence 16, Application US/10434364
; Publication No. US20040009554A1
; GENERAL INFORMATION:
; APPLICANT: WANG, DAGUANG
; TITLE OF INVENTION: QM-7 AND QT-6 CELLS TRANSFECTED WITH MUTANT CELL
; TITLE OF INVENTION: SURFACE EXPRESSED CHANNEL RECEPTORS AND ASSAYS USING
; FILE REFERENCE: MEMORY-11
; CURRENT APPLICATION NUMBER: US/10/434,364
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/378,642
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1367
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-1367

Query Match 27.3%; Score 512.2; DB 15; Length 968;
Best Local Similarity 90.1%; Pred. No. 2.4e-144;
Matches 608; Conservative 6; Mismatches 54; Indels 7; Gaps 6;

QY 1198 CCGCGCCGCGCCAGCAACGCGGACCTGCTACATCGGCTTCGCGGCTTCGACGCGCGCTG 1257
Db 8 CCCCCCCCCCAGTACAGGAAAGTGTTCACATCGCTTCGCGGCGCGCTGCGCGCTG 66
QY 1258 CACTGTGTCCCGACCCCGGACTCTCGGGTAGTGTGTGCGCGCATGGCGCTGCTCCCGCAG 1317
Db 67 CACTGTTCGCGACCCCGGACTCTCGGGTAGTGTGTGCGCGCATGGCGCTGCTCCCGCAG 126
QY 1318 CAGC-ATGAGGACCTCTGCGCGGCGGCAACCCCGGAGGGGACCCGAGCTTGGCCAA 1376
Db 127 CAGGAATGAACACCCCTTAACCGCGGCGGCAAAAAACCGAGGGGAAACCCGAGCTGGCCAA 186
QY 1377 GATCCTGGAGGAGTCCGCTACATTCGCAATCGCTTCGCTGCCAGGACGAAAGGAGCG 1436
Db 187 AATCCTG--AGAGTCCGCTACATTCGCCAA-MGYKTCGCTGCCA-KACGAAAGCGAGSC 242
QY 1437 GGTGTGCGAGGAGTGGAGTTCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1496
Db 243 -GTCTGCGAGGAGTGGAGTTCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 301
QY 1497 CTCGGTCTTCAACATCATCTGCACCATCGCATCCCTGATGTGGCTCCCAACTTCGTGGA 1556
Db 302 CTCGGTCTTCAACATCATCTGCACCATCGCATCCCTGATGTGGCTCCCAACTTCGTGGA 361
QY 1557 GCGCGGTCCAAAGACTTTGCGTAACACGCGCTGTTCTGTATCATGTGGAACCTCACAG 1616
Db 362 GCGCGGTCCAAAGACTTTGCGTAACACGCGCTGTTCTGTATCATGTGGAACCTCACAG 421
QY 1617 ATGGGCAAGGCTTTGCGTGGGAGATTGGGGGTGTCTAATCCAGGACGATTAACG 1676
Db 422 ATGGGCAAGGCTTTGCGTGGGAGATTGGGGGTGTCTAATCCAGGACGATTAACG 481
QY 1677 CCACACTCCAGTGTTCCTCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736
Db 482 CCACACTCCAGTGTTCCTCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
QY 1737 TTAGGTAGTAGAATCTCAGCACCTTTGTTTCATATTTCTCAGATGGGTGATAGATATCCTT 1796
Db 542 TTAGGTAGTAGAATCTCAGCACCTTTGTTTCATATTTCTCAGATGGGTGATAGATATCCTT 601
QY 1797 GGCACATCCGTAACATCGGTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1856
Db 602 GGCACATCCGTAACATCGGTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 661
QY 1857 TGCGTGGAAAGCCCT 1871
Db 662 TGCGTGGAAAGCCCT 676

RESULT 13
US-09-303-232-3
; Sequence 3, Application US/09303232A
; Patent No. US2002006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; TITLE OF INVENTION: Insect acetylcholine receptor subunits
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; EARLIER FILING DATE: 1999-04-30
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6

; SEQ ID NO 16
; LENGTH: 692
; TYPE: DNA
; ORGANISM: Macaca mulatta
US-10-434-364-16

Query Match 31.8%; Score 596.8; DB 16; Length 692;
Best Local Similarity 96.2%; Pred. No. 4.6e-170;
Matches 610; Conservative 1; Mismatches 23; Indels 0; Gaps 0;

QY 500 CAGGCAATTCAGAGTTCCTGCTACATCGATGTAGCTGTGTTCCCTTTGATGTGCAGC 559
Db 59 CCGGCAATTCAGAGTTCCTGCTACATCGATGTAGCTGTGTTCCCTTTGATGTGCAGC 118
QY 560 ACTGCAAACTGAAGTTGGTCTGCTCTTAAGAGGCTGTGCTTGGATCTGCAGATGC 619
Db 119 ATTGCAAACTGAAGTTGGTCTGCTCTTAAGAGGCTGTGCTTGGATCTGCAGATGC 178
QY 620 AGGAGGCAGATACAGTGGCTATATCCCAATGGAGATGGGACCTAGTGGGAATCCCG 679
Db 179 AGGAGGCAGATACAGTGGCTATATCCCAATGGAGATGGGACCTAGTGGGAATCCCG 238
QY 680 GCAAGAGGAGTGAAGGTTCTATGAGTGTCTGCAAGAGCCCTACCCGATGTCACTTCA 739
Db 239 GCAAGAGGAGTGAAGGTTCTATGAGTGTCTGCAAGAGCCCTACCCGATGTCACTTCA 298
QY 740 CAGTGACCATGCGCGGAGGACGCTCTACTATGGCTCAACCTGATCCCTGCTGTGC 799
Db 299 CAGTGACCATGCGCGGAGGACGCTCTACTATGGCTCAACCTGATCCCTGCTGTGC 358
QY 800 TCATCTCGGCGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
Db 359 TCATCTCGGCGCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
QY 860 CCTTGGGGAATAAGTCTTACTCTCTTACCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 919
Db 419 CCTTGGGGAATAAGTCTTACTCTCTTACCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 478
QY 920 TGCCCGCAACATCGATTCAGTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 979
Db 479 TGCCCGCAACATCGATTCAGTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
QY 980 TCGTGGGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1039
Db 539 TCGTGGGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 598
QY 1040 ACGGGGCAAGATCCCAAGTGGACAGAGTATCCTTCTGAACTGCTGCTGCTGCTGCTGCTGCT 1099
Db 599 ACGGGGCAAGATCCCAAGTGGACAGAGTATCCTTCTGAACTGCTGCTGCTGCTGCTGCTGCT 658
QY 1100 TSCGAATGAAGGCGCGGCGGAGGACAAAGTGGC 1133
Db 659 TSCGAATGAAGGCGCGGCGGAGGAGTAAGTGGC 692

RESULT 12
US-10-106-698-1367
; Sequence 1367, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0

144 ACCCTTGGAGAGCGCGTGGCAATGATCGCAACCGCTCACCGTCTACTTCTCCCTGA 203
245 GCCTCTGCAGATCATGAGCGTGGATGAGAGCAACCAAGTTTAAACCAACCAATTTGGC 304
204 GCCTCTGCAGATCATGAGCGCGGATGAGAGCAACCAAGTTTAAACCAACCAATTTGGC 263
305 TGCAAAATGCTTGGACAGATCACTATTATTACAGTGGGAATGTGTCAGAAATATCCAGGGGTGA 364
264 TGAATATGCTTGGACAGATCACTATTATTACAGTGGGAATGTGTCAGAAATATCCAGGGGTGA 323
365 AGACTGTTCTTCCAGATGGCGAGATTTGGAACCAAGCAATTTCTTCTTATAACAGTG 424
324 AGACTGTTCTTCCAGATGGCGAGATTTGGAACCAAGCAATTTCTTCTTATAACAGTG 383
425 CTGATGAGCGCTTGGACGACATTCACACTACAGTGGTGGTGAATTTCTTGGGCAT 484
384 CGGATGAGCGCTTGGACGACATTCACACTACAGTGGTGGTGAATTTCTTGGGCAT 443
485 GCCAGTACCTGCCCTCCAGGCATATTCAGAGTTCCTGCTA 524
444 GCCAGTACCTGCCCTCCAGGCATATTCAGAGTTCCTGCTA 483

RESULT 15

US-09-303-232-5

; Sequence 5, Application US/09303232A

; Patent No. US20020006657A1

; GENERAL INFORMATION:

; APPLICANT: Bayer Aktiengesellschaft

; TITLE OF INVENTION: Nucleic Acids which encode

; FILE OF INVENTION: insect acetylcholine receptor subunits

; FILE REFERENCE: Le A 33 020- Foreign Countries

; CURRENT APPLICATION NUMBER: US/09/303,232A

; CURRENT FILING DATE: 1999-04-30

; EARLIER APPLICATION NUMBER: DE 198 19 829.9

; EARLIER FILING DATE: 1998-05-04

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 3109

; TYPE: DNA

; ORGANISM: Heliothis virescens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (95)...(1597)

US-09-303-232-5

Query Match 20.0%; Score 376; DB 9; Length 3109;

Best Local Similarity 54.9%; Pred. No. 8.5e-103;

Matches 817; Conservative 1; Mismatches 646; Indels 24; Gaps 3;

QY 114 GTCGCTCTGCACGCTGTCCTGCAAGCGAGTTCCAGAGGAGCTTTACAGGAGCTGGT 173
DB 127 GCGTTTGTCTGCCGATCGAGCAAGTCTCAGCGAGAGACTTCTGNAACGCTTGT 186
QY 174 CAAGAATAACAATCCCTTGGAGAGCGCGTGGCCAAATGATCGCAACCACTCACCGTCTA 233
DB 187 GCGGAATAACAACCTTGGAGCGAGCGCGTGGCCAAAGAGAGCAACCGCTAGAGGTGAG 246
QY 234 CTTCTCCCTGAGCTCTCAGATCATGACGTGGATGAGAGACCAAGTTTAAACCA 293
DB 247 GTTCGGCTTGACCTTGCAGCAATCATTCACGTGGACGAGAGAAATCAACTACTTATAAC 306
QY 294 CAACATTTGGCTGCAATGCTTTGGACAGATCACTATTTACAGTGGAAATGTGTCAGAAATA 353
DB 307 CAATATATGGCTGCTGTTGGATGGGAATGACTTAACTTACCTGAGGTGGAAAGCAGCGAGTA 366
QY 354 TCCAGGGGTGAAGACTGTTCTGTTTCCAGATGGCCAGATTTGGAACCAAGCAATTTCT 413
DB 367 TGGCGGGGTCAAGGACCTCAGGATCAGCCCAAGATTTGGAGAGCGGACGTCCTTAT 426
QY 414 CTATAACAGTGTGATGAGCGCTTTTGACGCCCACTTCCACACTAAGCTGTGTGTAATTC 473

DB 427 GTATAATAGTGTGACGAGGGTTTACCGGAGCTTACACAGCAACAGCTGGTGTGAGAAG 486
QY 474 TTCTGGGCATTCGCAAGTACTGCTCTCCAGSCATATTCAAGAGTTCCTGTACATCGATGT 533
DB 487 CGCGGCGAGTTGCTGTACGTGCCACTTGCATATTCGAAGAGCACATGCAAGATGACAT 546
QY 534 AGCTGTTTCCCTTTGATGTGAGACACTGCAAACTGAAGTTTGGTCTGCTTACCG 593
DB 547 CGCGTGGTTCCCTTCCAGCAACCACTGTATATGAAGTTTGGTAGCTGGACATATGA 606
QY 594 AGCTGCTCTTGGATCTCAGATGAGGA-----GGCAGATATCAGTGGCTATAT 644
DB 607 CGCAATATCAGTTGATGCTGTGCTGCTAAAGATGAGGCGAGGCGGATCTATCGACTTCAT 666
QY 645 CCCCAATGAGAGATGGGACCTTAGTGGGAATCCCGGCAAGAGAGGTGAAGTTCTATGA 704
DB 667 AACCAATGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAGAACACATAACATACGC 726
QY 705 GTGCTGAAAGAGCCCTTACCCGATGTCACTTCACTGATGACCATGCGCGCAGGAGCT 764
DB 727 GTGCTGCCGAGCCCTTACGTTGACGCTTCACTTCACTGATGATGATGATGATGATGAT 786
QY 765 CTACTATGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCGCCCTCGCTGCTGCT 824
DB 787 GTACTTCTTCTCACTGATGCTCCGTCGCTGCTGATCTCATCGATGCACTTCTCTATC 846
QY 825 GTTCTGCTTCTGTCAGATTCGCGGAGAGATTTCCCTGGGATACAGTCTTACTCTC 884
DB 847 CTTTCACTGCCACAGACTCCGAGAGAAATCACACTTGGAGTCACTATTCTTCTATC 906
QY 885 TCTTACCGTCTTCTGCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 944
DB 907 GCTGACGCTGCTTCTCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
QY 945 ATTGATAGCCAGTACTTCCGACAGCACTGATCATCTGGGCTCTCGGTGGTGGTAC 1004
DB 967 CTTGTTAGGAGCTTCTTCAATTGATGATGATGATGATGATGATGATGATGATGATGAT 1026
QY 1005 GGTGATCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1064
DB 1027 TGTGTTGCTTCTCAATTTACCACCATGATGATGATGATGATGATGATGATGATGATGAT 1086
QY 1065 CAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1124
DB 1087 AAAATCAGTATTTCTCAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 1125 CAAGTGTGCGCGCTGCCAGCAACAGCGCGCTGCGAGCTGCGAGCTGCGAGTGGAGAT 1184
DB 1147 GATCACAGGAGAGACTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1206
QY 1185 GAGCGCGTGGCG 1244
DB 1207 GTCGTGCAAGTCTTGTGTCGCGAATGTTCTAGATATGATGATGATGATGATGATGATGAT 1266
QY 1245 CTTGAGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
DB 1267 TCGCGCTCTTAAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
QY 1303 GCCTGCTCCCCCAGCAGATGAGCACTCTGCAAGCGCGGCAACCCCGCGAGGGG-- 1360
DB 1327 CACGATTTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
QY 1361 -----ACCGGACTTGGCCAGATCTCGAGGAGTTCGCTACATTTGCCAATCG 1409
DB 1387 GGTAGGCCACCATCGCGAGCTGCACCTTACTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1446
QY 1410 CTTTCCGCTGCCAGGAGAAAGCGAGCGCTGTGCGAGCGAGTGGAAAGTTTCGCGCGCTGTGT 1469
DB 1447 GATGAAGAGGCTGATGAGAGAGCGAGCTGATCAGCGACTGGAAGTTTGTGCGATGT 1506
QY 1470 GGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1529

us-09-703-951a-11.rnpb

Wed May 12 09:51:14 2004

Db 1507 TGTGATAGGTTTGGCTGTTGCTGTTTCACACTTTTCAACAATCATCGCGACAGTAGCTGT 1566

Qy 1530 CCTGATGTCGGCTCCCAACTTCTGAGGCGCGTGTCCAAAGACTTTGC 1577

Db 1567 CCTGTTATCGGCACCGCATATCATCGTCAATGAACCAACCACCTGAGC 1614

Search completed: May 9, 2004, 00:10:49
Job time : 845 secs

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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 18:04:23 ; Search time 150 Seconds
(without alignments)
6940.586 Million cell updates/sec

Title: US-09-703-951a-11

Perfect score: 1876

Sequence: 1 GCGCGAGCGCGAGCGCGG.....TGCCGTGAAGCCCTTGGGA 1876

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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2: /cgn2_6/prodata/2/ina/5B COMB.seq.*

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5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*

6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1875.6	100.0	1876	2	US-08-466-589-7
2	1875.6	100.0	1876	2	US-08-700-636-7
3	1875.6	100.0	1876	3	US-08-467-574-7
4	1875.6	100.0	1876	4	US-09-217-345-7
5	1875.6	100.0	1876	4	US-08-487-596-11
6	1875.6	100.0	1876	4	US-08-660-451A-11
7	1875.6	100.0	1876	4	US-08-892-985-7
8	1543	82.2	1590	4	US-08-771-737-1
9	1543	82.2	1590	4	US-09-954-936-1
10	362.2	19.3	2277	1	US-08-496-855A-1
11	362.2	19.3	2277	4	US-08-487-596-1
12	362.2	19.3	2664	4	US-08-660-451A-1
13	345.8	18.4	2068	4	US-08-466-589-1
14	345.8	18.4	2068	2	US-08-700-636-1
15	345.8	18.4	2068	3	US-08-467-574-1
16	345.8	18.4	2068	4	US-09-217-345-1
17	345.8	18.4	2068	4	US-08-892-985-1
18	304.8	16.2	3496	4	US-08-660-451A-5
19	295.2	15.7	2363	4	US-08-487-596-5
20	294.8	15.7	2374	2	US-08-466-589-5
21	294.8	15.7	2374	2	US-08-700-636-5
22	294.8	15.7	2374	3	US-08-467-574-5
23	294.8	15.7	2374	4	US-09-217-345-5
24	294.8	15.7	2374	4	US-08-892-985-5
25	291.8	15.6	1908	4	US-08-660-451A-3
26	284.6	15.2	1756	2	US-08-466-589-3
27	284.6	15.2	1756	2	US-08-700-636-3

28 284.6 15.2 1756 3 US-08-467-574-3 Sequence 3, Appli
29 284.6 15.2 1756 4 US-09-217-345-3 Sequence 3, Appli
30 284.6 15.2 1756 4 US-09-892-985-3 Sequence 3, Appli
31 279 14.9 1654 4 US-08-487-596-3 Sequence 3, Appli
32 275.4 14.7 1743 4 US-08-487-596-9 Sequence 9, Appli
33 275.4 14.7 1743 4 US-08-484-722-1 Sequence 1, Appli
34 275.4 14.7 1743 4 US-08-660-451A-9 Sequence 9, Appli
35 263.2 14.0 2448 4 US-08-487-596-13 Sequence 13, Appli
36 263.2 14.0 2448 4 US-08-660-451A-13 Sequence 13, Appli
37 263.2 14.0 2450 2 US-08-466-589-9 Sequence 9, Appli
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40 263.2 14.0 2450 4 US-09-217-345-9 Sequence 9, Appli
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42 261.6 13.9 1521 1 US-08-496-855A-3 Sequence 3, Appli
43 261.6 13.9 1521 2 US-07-938-154-9 Sequence 9, Appli
44 261.6 13.9 1521 5 PCT-US91-02311-9 Sequence 9, Appli
45 253.4 13.5 1915 4 US-08-487-596-17 Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-466-589-7
; Sequence 7, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & Mcclain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1876 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..1581
US-08-466-589-7

Query Match		100.0%;	Score 1875.6;	DB 2;	Length 1876;		
Best Local Similarity		100.0%;	Pred. No. 0;				
Matches 1876;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	1	GGCGCAGGCGCAGGCGCGCGCGCAGCAGCGAGAGCTGGAGCGCGCGCGCTGCGTGCAGCT	60				
Db	1	GGCGCAGGCGCAGGCGCGCGCGCAGCAGCGAGAGCTGGAGCGCGCGCGCTGCGTGCAGCT	60				
QY	61	CGGGAGCTCAACATCGGCTGCTCGCGGAGGCGTCTGGCTGGCGCTGGCGCGCTGCTGCTC	120				
Db	61	CGGGAGCTCAACATCGGCTGCTCGCGGAGGCGCTCTGGCTGGCGCTGGCGCGCTGCTGCTC	120				
QY	121	CTGCACTGTCCTCTCAAGGCGAGTTCAGAGGAAGCTTTACAGGAGCTGGTCAAGAAC	180				
Db	121	CTGCACTGTCCTCTCAAGGCGAGTTCAGAGGAAGCTTTACAGGAGCTGGTCAAGAAC	180				
QY	181	TACAACTCCCTTGGAGAGCGCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCC	240				
Db	181	TACAACTCCCTTGGAGAGGCGCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCC	240				
QY	241	CTGAGCCTCTGAGATCATGACCTGGATGAGAGAACCAAGTTTAAACCAACCAACTT	300				
Db	241	CTGAGCCTCTGAGATCATGACCTGGATGAGAGAACCAAGTTTAAACCAACCAACTT	300				
QY	301	TGGCTGCAAAATGCTTTGGACAGATCACTATTTACAGTGGAAATGTGTGAGAATATCCAGG	360				
Db	301	TGGCTGCAAAATGCTTTGGACAGATCACTATTTACAGTGGAAATGTGTGAGAATATCCAGG	360				
QY	361	GTGAAGACTGTGCTTCCAGATGCGCAGATTTGGAACCAAGACATTTCTCTATATAAC	420				
Db	361	GTGAAGACTGTGCTTCCAGATGCGCAGATTTGGAACCAAGACATTTCTCTATATAAC	420				
QY	421	AGTGTGATGAGCGCTTTGACGCGCACTTTCCACACTTAACGTGTGTGTGAAATTTCTTGG	480				
Db	421	AGTGTGATGAGCGCTTTGACGCGCACTTTCCACACTTAACGTGTGTGTGAAATTTCTTGG	480				
QY	481	CATTGCCAGTACCTGCTCCAGGCAATTAAGAGTTCCTGCTACATCGATGTCAGCTGG	540				
Db	481	CATTGCCAGTACCTGCTCCAGGCAATTAAGAGTTCCTGCTACATCGATGTCAGCTGG	540				
QY	541	TTTCCCTTTGATGTCAGCACTGCAAACTGAATTTGGGTCTGTGGTCTTACGGAGCTGG	600				
Db	541	TTTCCCTTTGATGTCAGCACTGCAAACTGAATTTGGGTCTGTGGTCTTACGGAGCTGG	600				
QY	601	TCCTTGGATCTGCAATGCAAGGAGCAGATATCAGTGGCTATATCCCAATGGAGAATGG	660				
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QY	721	TACCCGATGTCACCTTCCAGTGAACATGCGCGAGGAGCTCTACTATGGCGCTCAAC	780				
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QY	781	CTGCTGATCCCTGTGTGCTCATCTCGCGCTCGCCCTGCTGCTGCTGCTGCTGCTGCA	840				
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QY	841	GATTCGGGGAGAGATTTCCCTGGGATTAACAGTCTTACTCTCTCTTACCGTCTTCATG	900				
Db	841	GATTCGGGGAGAGATTTCCCTGGGATTAACAGTCTTACTCTCTTACCGTCTTCATG	900				
QY	901	CTGCTCGTGGCTGAGATCATGCGCGCAACATCCGATTCGGTACCATGATAGCCCAAGTAC	960				
Db	901	CTGCTCGTGGCTGAGATCATGCGCGCAACATCCGATTCGGTACCATGATAGCCCAAGTAC	960				
QY	961	TTGCGCAGCACCATGATCATCTGCGGCTCTCGGTGGTGGTGAAGCGTATGCTGCTGCGAG	1020				
Db	961	TTGCGCAGCACCATGATCATCTGCGGCTCTCGGTGGTGGTGAAGCGTATGCTGCTGCGAG	1020				
QY	1021	TACCACCAACGACCCCGACGGGGGCAAGATGCCCAAGTGGACCAAGATCATCTTCTTG	1080				

Db	1021	TACCACCAACGACCCCGACGGGGCAAGATGCCCAAGTGGACCAAGATCATCTTCTG	1080				
QY	1081	AACCTGTGCGCGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG	1140				
Db	1081	AACCTGTGCGCGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG	1140				
QY	1141	TGCGACCAACGACGCGCGCTGCGCTTGGCAGTGTGGAGATGAGCGCGTGGCGCG	1200				
Db	1141	TGCGACCAACGACGCGCGCTGCGCTTGGCAGTGTGGAGATGAGCGCGTGGCGCG	1200				
QY	1201	CCGCGCGCGACGAAACGCGAACTTGTGTATCGGCTTCCGCGGCTTGGACGCGTGCAC	1260				
Db	1201	CCGCGCGCGACGAAACGCGAACTTGTGTATCGGCTTCCGCGGCTTGGACGCGTGCAC	1260				
QY	1261	TGTGTCCCGACCCCGACTCTGGGCTAGTGTGTGGCGCATGCGCTTCTCCCGACGSCAC	1320				
Db	1261	TGTGTCCCGACCCCGACTCTGGGCTAGTGTGTGGCGCATGCGCTTCTCCCGACGSCAC	1320				
QY	1321	GATGAGCACCTCTGCAACGCGCGGCAACCCCGAGGGGACCCGGAATTTGGCCCAAGATC	1380				
Db	1321	GATGAGCACCTCTGCAACGCGCGGCAACCCCGAGGGGACCCGGAATTTGGCCCAAGATC	1380				
QY	1381	CTGAGGAGTCTCGCTACATTCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCG	1440				
Db	1381	CTGAGGAGTCTCGCTACATTCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCG	1440				
QY	1441	TGCGACGAGTGAAGTTCGCGCGCTGCTGTGTGGACCGCTTCTGCTTCTGCTTCTG	1500				
Db	1441	TGCGACGAGTGAAGTTCGCGCGCTGCTGTGTGGACCGCTTCTGCTTCTGCTTCTG	1500				
QY	1501	GTCTTACCAATCTGCAACATCGGCACTGCTGTGTGGACCGCTTCTGCTTCTGCTTCTG	1560				
Db	1501	GTCTTACCAATCTGCAACATCGGCACTGCTGTGTGGACCGCTTCTGCTTCTGCTTCTG	1560				
QY	1561	GTGTCCAAAGACTTTGGGTAAACCAACGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT	1620				
Db	1561	GTGTCCAAAGACTTTGGGTAAACCAACGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT	1620				
QY	1621	GCAAGGCTTTGGCTTGGCGAGATTTGGGGGTGTAAATCCAGGACAGCATTTACAGCCAC	1680				
Db	1621	GCAAGGCTTTGGCTTGGCGAGATTTGGGGGTGTAAATCCAGGACAGCATTTACAGCCAC	1680				
QY	1681	AACCTCAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740				
Db	1681	AACCTCAGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740				
QY	1741	GTAGTAGAATCTCAGCACTTTGTTTCTATATTTCTCAGATGGCTCATAGATATCTTGGCA	1800				
Db	1741	GTAGTAGAATCTCAGCACTTTGTTTCTATATTTCTCAGATGGCTCATAGATATCTTGGCA	1800				
QY	1801	CATCCGTACCATCGGTGAGAGGCGCACTGAGTGTGATTTTGGCCATTTAGCCCACTGCC	1860				
Db	1801	CATCCGTACCATCGGTGAGAGGCGCACTGAGTGTGATTTTGGCCATTTAGCCCACTGCC	1860				
QY	1861	TGGAAGGCTTCCGA 1876					
Db	1861	TGGAAGGCTTCCGA 1876					

RESULT 2
US-08-700-636-7
; Sequence 7, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Elliot, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,636
FILING DATE: 16-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 73..1581
US-08-700-636-7

Query Match 100.0%; Score 1875.6; DB 2; Length 1876;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGCCGACGCGCAGCGCCGGGCGAGCCGACGCTGGAGCGCGCGCTCGCTCAGCT	60
DB	1	GGCCGACGCGCAGCGCCGGGCGAGCCGACGCTGGAGCGCGCGCTCGCTCAGCT	60
QY	61	CGGGAATCAACATCGCTGCTCGCGGAGCGCTGCTGCGCGCTGCGCGCTCGCTC	120
DB	61	CGGGAATCAACATCGCTGCTCGCGGAGCGCTGCTGCGCGCTGCGCGCTCGCTC	120
QY	121	CTGCACTGCTCCCTCGACGCGAGTTCCAGAGGAGCTTTACAGGAGCTGGTCAAGAC	180
DB	121	CTGCACTGCTCCCTCGACGCGAGTTCCAGAGGAGCTTTACAGGAGCTGGTCAAGAC	180
QY	181	TACAATCCCTTGGAGGCGCGTGGCCAAATGACTCGCAACCACTCAACGCTTCTCC	240
DB	181	TACAATCCCTTGGAGGCGCGTGGCCAAATGACTCGCAACCACTCAACGCTTCTCC	240
QY	241	CTGAGCTCTCGAGATCAATGAGCGTGGATGAGAACCAAGTTTAAACCAACATTT	300
DB	241	CTGAGCTCTCGAGATCAATGAGCGTGGATGAGAACCAAGTTTAAACCAACATTT	300
QY	301	TGGCTGCAATGCTTGGACAGATCACTATTTACAGTGAATGTGTGAGAAATATCCAGG	360
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QY	361	GTGAAGCTGTTCTGTTCCAGATGCGCAGATTGGAACCAACAGACATTTCTCTATAAC	420
DB	361	GTGAAGCTGTTCTGTTCCAGATGCGCAGATTGGAACCAACAGACATTTCTCTATAAC	420
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DB	421	AGTGTGATGAGCGCTTTGAGCGCCACATTCACATCAACATGCTGTGTGTAATCTTGGG	480
QY	481	CATTGCCAGTACTGCTCCAGGCATATTCAAGAGTTCTGCTACATCATGATGACGTGG	540

DB	481	CATTGCCAGTACTGCTCCAGGCATATTCAAGAGTTCTGCTACATCATGATGACGTGG	540
QY	541	TTTCCCTTTGATGTGACGACCTGCAAACTGAAGTTTGGTCTCTGCTTTACGAGGCTGG	600
DB	541	TTTCCCTTTGATGTGACGACCTGCAAACTGAAGTTTGGTCTCTGCTTTACGAGGCTGG	600
QY	601	TCCTTGGATCTGACAGATGACAGAGGACAGATATCAGTGGCTATATCCCAATGGAGAATGG	660
DB	601	TCCTTGGATCTGACAGATGACAGAGGACAGATATCAGTGGCTATATCCCAATGGAGAATGG	660
QY	661	GACCTAGTGGAAATCCCGGCAAGAGAGTGAAGTTCTATGATGCTGCAAAAGAGCCC	720
DB	661	GACCTAGTGGAAATCCCGGCAAGAGAGTGAAGTTCTATGATGCTGCAAAAGAGCCC	720
QY	721	TACCCGATGTCACTTCACAGTCAACATGCGCGCAGAGCGCTCTACTATGGCTCAAC	780
DB	721	TACCCGATGTCACTTCACAGTCAACATGCGCGCAGAGCGCTCTACTATGGCTCAAC	780
QY	781	CTGCTGATCCCTGTGTGCTCATCTCGCCCTCGCCCTGCTGCTGCTTCTCTGCTGCA	840
DB	781	CTGCTGATCCCTGTGTGCTCATCTCGCCCTCGCCCTGCTGCTGCTTCTCTGCTGCA	840
QY	841	GATTCCGGGAGAGATTTCCCTGGGATACAGTCTTACTCTCTCTCTCTCTCTCTCTCT	900
DB	841	GATTCCGGGAGAGATTTCCCTGGGATACAGTCTTACTCTCTCTCTCTCTCTCTCTCT	900
QY	901	CTGCTCGTGGCTGAGATCATGCGCCCAACATCCGATTCGATACCAATTGATAGCCAGTAC	960
DB	901	CTGCTCGTGGCTGAGATCATGCGCCCAACATCCGATTCGATACCAATTGATAGCCAGTAC	960
QY	961	TTGCGCAGACCATGATCATCTGCGGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTG	1020
DB	961	TTGCGCAGACCATGATCATCTGCGGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTG	1020
QY	1021	TACCAACACACGACCGCGGAGAGATGCCAAAGTGGACAGAGTCACTCTCTCTCTCT	1080
DB	1021	TACCAACACACGACCGCGGAGAGATGCCAAAGTGGACAGAGTCACTCTCTCTCTCT	1080
QY	1081	AATCGTGGCTGCTGCTCTSCAATGAAGAGGCGCGGAGGAGCAAGTGTGCGCGCGCC	1140
DB	1081	AATCGTGGCTGCTGCTCTSCAATGAAGAGGCGCGGAGGAGCAAGTGTGCGCGCGCC	1140
QY	1141	TGCGACACAAAGAGCGCGCTGACGCTGCGAGTGTGAGATGAGCGCGCTGCGCGCG	1200
DB	1141	TGCGACACAAAGAGCGCGCTGACGCTGCGAGTGTGAGATGAGCGCGCTGCGCGCG	1200
QY	1201	CGCGCGCGCAGCAACGAGAACTGCTGTACATCGGCTTCCGCGGCTGGAAGCGCTGAC	1260
DB	1201	CGCGCGCGCAGCAACGAGAACTGCTGTACATCGGCTTCCGCGGCTGGAAGCGCTGAC	1260
QY	1261	TGTGTCCGACCCCGACTCTGGGTAGTGTGTGCGCGATGGCTGTCTCCCGACGAC	1320
DB	1261	TGTGTCCGACCCCGACTCTGGGTAGTGTGTGCGCGATGGCTGTCTCCCGACGAC	1320
QY	1321	GATGACACCTCTGACGCGGCGCAACCCCGGAGGAGGAGCCCGACTTGGCGCAGATC	1380
DB	1321	GATGACACCTCTCTGACGCGGCGCAACCCCGGAGGAGGAGCCCGACTTGGCGCAGATC	1380
QY	1381	CTGAGGAGGCTCCGCTTACATTCGCTTCCGCTGCGAGAGCAAGAGCGAGCGCTC	1440
DB	1381	CTGAGGAGGCTCCGCTTACATTCGCTTCCGCTGCGAGAGCAAGAGCGAGCGCTC	1440
QY	1441	TGACGAGTGAAGTTTCCGCGCTGTGTGAGACCGCTGTGTCTCATGAGCTTCTGG	1500
DB	1441	TGACGAGTGAAGTTTCCGCGCTGTGTGAGACCGCTGTGTCTCATGAGCTTCTGG	1500
QY	1501	GTCTTCAACATCATCTGACCATCGGCTCTGATGCTGGCTCCCACTTCTGAGGCG	1560
DB	1501	GTCTTCAACATCATCTGACCATCGGCTCTGATGCTGGCTCCCACTTCTGAGGCG	1560
QY	1561	GTGTCGAAGAGCTTTGCGTAAACCGCTGCTGTTCTGTATCATGTGGAATCTCACAGATGG	1620

1561	GTGTCCAAAGACTTTGGGTAAACGACCGCTCGTGTCTGTATCATGTGGAAAACCTCACAGATGG	1520
1621	GCAAGGCGCTTTGGCTTGGCGAGATTTGGGGGTGCTAAATCCAGGACAGCAATTACACGCCAC	1680
1621	GCAAGGCGCTTTGGCTTGGCGAGATTTGGGGGTGCTAAATCCAGGACAGCAATTACACGCCAC	1680
1681	AACATCCAGTGTTCCTCTTCGGCTGCTCAGTCGTGTGCTACGGTTCCTTTGTTACTTTTAG	1740
1681	AACATCCAGTGTTCCTCTTCGGCTGCTCAGTCGTGTGCTACGGTTCCTTTGTTACTTTTAG	1740
1741	GTATGAGAAATCTCAGCACTTTGTTTTCATATTTCTCAGATGGGCTGATAGATATCTCTTGGCA	1800
1741	GTATGAGAAATCTCAGCACTTTGTTTTCATATTTCTCAGATGGGCTGATAGATATCTCTTGGCA	1800
1801	CATCCGTACCATTGGTTCAGCAGGGCCACTCAGTAGTCAATTTGCCCATTAGCCCACTGCC	1860
1801	CATCCGTACCATTGGTTCAGCAGGGCCACTCAGTAGTCAATTTGCCCATTAGCCCACTGCC	1860
1861	TGGAAGGCCCTTCGGA	1876
1861	TGGAAGGCCCTTCGGA	1876

RESULT 3

US-08-467-574-7
 ; Sequence 7, Application US/08467574
 ; Patent No. 6022704
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClaim
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467,574
 ; FILING DATE: June 5, 1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: March 8, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-9949
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1876 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 73..1581
 ; US-08-467-574-7

1021 TACCACACACAGACCCGACCGGGCAAGATGCCAAGTGCACAGAGTCATCTCTG 1080
1081 AACTGGTCGGGTGTTCTCTSCGATGAAGAGGCGCGGAGGACAAAGTGGCGCGGCC 1140
1081 AACTGGTCGGGTGTTCTCTSCGATGAAGAGGCGCGGAGGACAAAGTGGCGCGGCC 1140
1141 TGCCAGCACAGACAGCGCGGTGACAGCTGCGAGTGTGGAGATGAGCGCGGTGCGCGC 1200
1141 TGCCAGCACAGACAGCGCGGTGACAGCTGCGAGTGTGGAGATGAGCGCGGTGCGCGC 1200
1201 CGCGCCGACAGCAACCGGAACTGCTGTACATGCGCTTCGCGGCTGGAAGCGGTGAC 1260
1201 CGCGCCGACAGCAACCGGAACTGCTGTACATGCGCTTCGCGGCTGGAAGCGGTGAC 1260
1261 TGTCGCCAGACCCCGAGCTCTGGGTGAGTGTGGCGCATGGCTGCTCCCGACGAC 1320
1261 TGTCGCCAGACCCCGAGCTCTGGGTGAGTGTGGCGCATGGCTGCTCCCGACGAC 1320
1321 GATGAGCACCTCTGACGCGCGGCAACCCCGAGGGGACCCCGACTTGGCCAGATC 1380
1321 GATGAGCACCTCTGACGCGCGGCAACCCCGAGGGGACCCCGACTTGGCCAGATC 1380
1381 CTGAGAGAGTCCGTACATGCCAATCGCTTCGCTGCGAGCAAGAGCGAGCGGTG 1440
1381 CTGAGAGAGTCCGTACATGCCAATCGCTTCGCTGCGAGCAAGAGCGAGCGGTG 1440
1441 TGCCAGAGTGAAGTTCGCGCTGTGGTGGACCGCTGCTCATGSCCTTCTCG 1500
1441 TGCCAGAGTGAAGTTCGCGCTGTGGTGGACCGCTGCTCATGSCCTTCTCG 1500
1501 GTCTTACCACATCATGACACATCGCATCTGCTGCGCTCCCACTTCGTGGAGGC 1560
1501 GTCTTACCACATCATGACACATCGCATCTGCTGCGCTCCCACTTCGTGGAGGC 1560
1561 GTGTCGAAGACTTGGTAACACAGCGCTGTTCTGTACATGTGGAACCTCAGATGG 1620
1561 GTGTCGAAGACTTGGTAACACAGCGCTGTTCTGTACATGTGGAACCTCAGATGG 1620
1621 GCAAGGCTTTCGCTGGGAGATTGGGGGTGCTAATCCAGACAGCATTCACGCCAC 1680
1621 GCAAGGCTTTCGCTGGGAGATTGGGGGTGCTAATCCAGACAGCATTCACGCCAC 1680
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1681 AACTCCAGTTCCTCTGCGTGTGAGTGTGCTGTGCTTACGTTCTTTGTACTTTAG 1740
1741 GTAGTAGATCTCAGACATTTGTTTCAATTTCTCAGATGGGCTGATAGATATCCTGGCA 1800
1741 GTAGTAGATCTCAGACATTTGTTTCAATTTCTCAGATGGGCTGATAGATATCCTGGCA 1800
1801 CATCGTACCATCGGTGACAGGCGCACTGAGTAGTCAATTTGCGCCATTAGCCCACTGCC 1860
1801 CATCGTACCATCGGTGACAGGCGCACTGAGTAGTCAATTTGCGCCATTAGCCCACTGCC 1860
1861 TGAAGAGCCCTTCGGA 1876
1861 TGAAGAGCCCTTCGGA 1876

RESULT 4
US-09-217-345-7
; Sequence 7, Application US/09217345
; Patent No. 6303753
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe

STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 73..1581
US-09-217-345-7

Query Match 100.0%; Score 1875.6; DB 4; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSCCGCAGCGCAGCGCGCGCGCAGCGCGAGCGTGGAGCGCGCGCGCTCGCTGCGAGCT 60
Db 1 GSCCGCAGCGCAGCGCGCGCGCGCAGCGCGAGCGTGGAGCGCGCGCGCTCGCTGCGAGCT 60
QY 61 CCGGAGCTCAACATGCGTGTCTCGCGGAGCGCGTCTGCGTGGCGCGCGCGCTGCGCTGCTC 120
Db 61 CCGGAGCTCAACATGCGTGTCTCGCGGAGCGCGTCTGCGTGGCGCGCGCGCTGCGCTGCTC 120
QY 121 CTGACGCTGCTCCCTGCAAGCGAGTTCAGAGAGAGCTTTTACAAGAGAGCTGGTCAAGAAC 180
Db 121 CTGACGCTGCTCCCTGCAAGCGAGTTCAGAGAGAGCTTTTACAAGAGAGCTGGTCAAGAAC 180
QY 181 TACAATCCCTTGGAGAGCGCGCGTGGCCATGATGCTGCGCCATGATGCTGCGCTTCTCTCC 240
Db 181 TACAATCCCTTGGAGAGCGCGCGTGGCCATGATGCTGCGCCATGATGCTGCGCTTCTCTCC 240
QY 241 CTGAGCTCTCTGAGATCATGAGCGTGGATGAGAGAGCAAGTTTAAACCAACCAAT 300
Db 241 CTGAGCTCTCTGAGATCATGAGCGTGGATGAGAGAGCAAGTTTAAACCAACCAAT 300
QY 301 TGGCTGCAATGCTTGGAGAGCTTACATTTTACAGTGAATGTGTGAGATATCCAGGG 360
Db 301 TGGCTGCAATGCTTGGAGAGCTTACATTTTACAGTGAATGTGTGAGATATCCAGGG 360
QY 361 GTGAGAGCTGCTGCTTCCAGATGCGCAGATTTGGAAACCAAGACATTTCTTCTATAAC 420
Db 361 GTGAGAGCTGCTGCTTCCAGATGCGCAGATTTGGAAACCAAGACATTTCTTCTATAAC 420

421 AGTGTGATGAGCGCTTTGACGGCCACATTCCACATAACGTGTGTGTAATCTTCTGGG 480
Db
421 AGTGTGATGAGCGCTTTGACGGCCACATTCCACATAACGTGTGTGTAATCTTCTGGG 480
QY 481 CATTGCCAGTACCTGCTCCAGGCATATTCAGAGTTCCTGTACATCGATGACGCTGG 540
Db 481 CATTGCCAGTACCTGCTCCAGGCATATTCAGAGTTCCTGTACATCGATGACGCTGG 540
QY 541 TTTCCCTTTGATGTGACAGCACTGCAAACTGAAGTTTGGGTCTGTGTTTACGAGGCTGG 600
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QY 601 TCCTTGATCTCAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGAGAGATGG 660
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QY 661 GACCTAGTGGAAATCCCGGCAAGAGAGGTGAAAGTTTCTATGAGTCTGCAAGAGCCC 720
Db 661 GACCTAGTGGAAATCCCGGCAAGAGAGGTGAAAGTTTCTATGAGTCTGCAAGAGCCC 720
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Db 721 TACCCCGATGACCTTCAAGTGAACATGCGCGCAGAGCGCTCTACTATGGCCTCAAC 780
QY 781 CTGCTGATCCCTGTGTGCTCATCTCCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCA 840
Db 781 CTGCTGATCCCTGTGTGCTCATCTCCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCA 840
QY 841 GATTCCGGGAGAGAAATTTCCCTGGGATACAGTCTTACTCTCTCTTACCGTCTCATG 900
Db 841 GATTCCGGGAGAGAAATTTCCCTGGGATACAGTCTTACTCTCTCTTACCGTCTCATG 900
QY 901 CTGCTGCTGTGATGATCATGCCCGCAACATCCGATTCGTTACCATGATAGCCAGTAC 960
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QY 961 TTCCCGCAGCACCATGATCATGCTGGGCTCTCGGTGGTGTGAGCGTGTGCTGCTGCG 1020
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QY 1021 TACCACCAACAGACCCCGAGCGGCGAAGATGCCCCAAGTGGACAGAGTCACTCTTCTG 1080
Db 1021 TACCACCAACAGACCCCGAGCGGCGAAGATGCCCCAAGTGGACAGAGTCACTCTTCTG 1080
QY 1081 AACTGCTGCGGTGTTCTCTGATGAAAGGCGCGGAGGAGCAAGTGGCGCGCGCC 1140
Db 1081 AACTGCTGCGGTGTTCTCTGATGAAAGGCGCGGAGGAGCAAGTGGCGCGCGCC 1140
QY 1141 TGCCAGACACAGCAGCGCGCTGACGCTGCGCAGTGTGGAGATGAGCGCGCTGGCGCG 1200
Db 1141 TGCCAGACACAGCAGCGCGCTGACGCTGCGCAGTGTGGAGATGAGCGCGCTGGCGCG 1200
QY 1201 CGCCCGCGCAGCAACGCGAACTGTGTATGAGTTCGCGGCTGCGGCGCTGAGCGCGTGCAC 1260
Db 1201 CGCCCGCGCAGCAACGCGAACTGTGTATGAGTTCGCGGCTGCGGCGCTGAGCGCGTGCAC 1260
QY 1261 TGTGTCCCGACCCCGACTCTGGGTGAGTGTGCGCGCATGCTGCTCCCGCAGCGAC 1320
Db 1261 TGTGTCCCGACCCCGACTCTGGGTGAGTGTGCGCGCATGCTGCTCCCGCAGCGAC 1320
QY 1321 GATGAGCACTCTGCAAGCGGCGCAACCCCGCGAGGAGGACCCGAGCTTGGCCAGATC 1380
Db 1321 GATGAGCACTCTGCAAGCGGCGCAACCCCGCGAGGAGGACCCGAGCTTGGCCAGATC 1380
QY 1381 CTGGAGGAGGTCCGCTTACATGTCATTCGCTTCCGCTGCGAGGACGAAAGCGAGCGCTC 1440
Db 1381 CTGGAGGAGGTCCGCTTACATGTCATTCGCTTCCGCTGCGAGGACGAAAGCGAGCGCTC 1440
QY 1441 TGCAGCGAGTGAAGTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Db 1441 TGCAGCGAGTGAAGTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500

QY 1501 GTCTTCACCATCATCTGCACCATCGGATCTCTGATGTGTGGCTCCCAACTTCGTGGAGGCC 1560
Db 1501 GTCTTCACCATCATCTGCACCATCGGATCTCTGATGTGTGGCTCCCAACTTCGTGGAGGCC 1560
QY 1561 GTGTCCAAAGACTTTGCGTTAAACACGCGCTGTTCTGTACATGTGGAAACTCACAGATGG 1620
Db 1561 GTGTCCAAAGACTTTGCGTTAAACACGCGCTGTTCTGTACATGTGGAAACTCACAGATGG 1620
QY 1621 GCAAGGCTTTGCTTGGCGAGATTTGGGGGTGCTAAATCCAGGACAGCAATTAACGCCAC 1680
Db 1621 GCAAGGCTTTGCTTGGCGAGATTTGGGGGTGCTAAATCCAGGACAGCAATTAACGCCAC 1680
QY 1681 AACTCCAGTGTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 AACTCCAGTGTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1741 GTAGTGAATCTCAGACATTTGTTTCATATTTCTCAGATGGGCTGATAGATATCTTTGGCA 1800
Db 1741 GTAGTGAATCTCAGACATTTGTTTCATATTTCTCAGATGGGCTGATAGATATCTTTGGCA 1800
QY 1801 CATCCGTACCATCGGTACGAGGCGCCACTGAGTAGTCAATTTGCCCATGAGCCACTGCC 1860
Db 1801 CATCCGTACCATCGGTACGAGGCGCCACTGAGTAGTCAATTTGCCCATGAGCCACTGCC 1860
QY 1861 TGGAAAGCCCTTCGGA 1876
Db 1861 TGGAAAGCCCTTCGGA 1876

RESULT 5
US-08-487-596-11
; Sequence 11, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:

QY 1861 TGAAGAGCCCTTCGGA 1876
Db 1861 TGAAGAGCCCTTCGGA 1876

RESULT 6
US-08-660-451A-11
Sequence 11, Application US/08660451A
Patent No. 6524789
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 73...1581
OTHER INFORMATION: alpha7 human neuronal nicotinic
receptor
NAME/KEY: 5'UTR
LOCATION: 1...72
OTHER INFORMATION:
NAME/KEY: 3'UTR
LOCATION: 1582...1876
OTHER INFORMATION:
US-08-660-451A-11

Query Match 100.0%; Score 1875.6; DB 4; Length 1876;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1875; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCGCAGGCGCAGGCGCGCGCGCAGCGGAGACGCTGGAGCGCGCGCGCTCCCTGCAGCT 60

61 CCGGACTCAACATCGCTGCTCGCGCGGAGCGCTCTGGCTGGCGCTGGCGCGCTGGCTC 120

61 CCGGACTCAACATCGCTGCTCGCGGAGCGCTCTGGCTGGCGCTGGCGCGCTGGCTC 120

121 CTGCACGTGTCCCTGCAAGCGAGTTTCAGAGGAGCTTTTACAGGAGCTGGTCAAGAAC 180

121 CTGCACGTGTCCCTGCAAGCGAGTTTCAGAGGAGCTTTTACAGGAGCTGGTCAAGAAC 180

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361 GTGAAGACTGTTTCCAGATGCGCAGATTTGGAACCAAGACATTTCTTCTATAAC 420

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421 AGTGTGATGAGCGCTTTGACGCCACATTCACATTAACGTGTGGTGAATTTCTTCTGGG 480

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901 CTGCTCGTGGTGGATCATGCGCGCAACATCCGATTCGGTACCAATGATGAGCCAGTAC 960

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1021 TACGACCAACCGAGCCCGGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 1080

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1081 AACTGGTGGCTGGTTCCTTCTGCAATGAAGAGCGCGCGGAGGACAAGAGTGGCGCGCC 1140

1141 TGCCAGCAAGCAGCGCGCTGCAGCCTGCGCAGTGTGGAGATGAGCGCGTGGCGCG 1200
1141 TGCCAGCAAGCAGCGCGCTGCAGCCTGCGCAGTGTGGAGATGAGCGCGTGGCGCG 1200
1201 CGCCCGCCAGCAACGCGGAACTGTCTGATCGGCTTCCGCGCTCGAGCGGCTGCAC 1260
1201 CGCCCGCCAGCAACGCGGAACTGTCTGATCGGCTTCCGCGCTCGAGCGGCTGCAC 1260
1261 TGCTGCCGACCCCGACTCTGGGCTAGTGTGGCGCGCATGGCTGCTCCCGCAGCAC 1320
1261 TGCTGCCGACCCCGACTCTGGGCTAGTGTGGCGCGCATGGCTGCTCCCGCAGCAC 1320
1321 GATGAGCACTCTGCAAGCGGCGCAACCCCGCGAGGGGAGCCCGGACTTGGCGAGATC 1380
1321 GATGAGCACTCTGCAAGCGGCGCAACCCCGCGAGGGGAGCCCGGACTTGGCGAGATC 1380
1381 CTGGAGGAGTCCGCTACATTCGCAATCGCTTCGCTGCGCAGGACGAAAGCGAGCGGTC 1440
1381 CTGGAGGAGTCCGCTACATTCGCAATCGCTTCGCTGCGCAGGACGAAAGCGAGCGGTC 1440
1441 TGCAGCGAGTGAAGTTCGCGGCTGCTGGGCTGCTGGGCTGCTGCTGCTGCTGCTGCTG 1500
1441 TGCAGCGAGTGAAGTTCGCGGCTGCTGGGCTGCTGGGCTGCTGCTGCTGCTGCTGCTG 1500
1501 GTCTTCACCATCATCTGCACCATCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
1501 GTCTTCACCATCATCTGCACCATCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
1561 GTGTCCAAAGACTTTCGCTGCAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
1561 GTGTCCAAAGACTTTCGCTGCAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
1621 GCAAGCGCTTTCGCTGCGGAGATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
1621 GCAAGCGCTTTCGCTGCGGAGATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
1681 AACTCCAGTGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
1681 AACTCCAGTGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
1741 GTAGTAGAATCTCAGCACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
1741 GTAGTAGAATCTCAGCACTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
1801 CATCGTACATCGTGCAGCGGCGCACTGAGTAGTATTTGCGGCTGAGTATTTGCGGCTG 1860
1801 CATCGTACATCGTGCAGCGGCGCACTGAGTAGTATTTGCGGCTGAGTATTTGCGGCTG 1860
1861 TGGAAAGCCCTTCGGA 1876
1861 TGGAAAGCCCTTCGGA 1876

RESULT 7
US-09-892-985-7
; Sequence 7, Application US/09892985
; Patent No. 6664375
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,985
FILING DATE: 27-Jun-2001
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 73..1581
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-892-985-7
Query Match 100.0%; Score 1875.6; DB 4; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGCCAGCGCGCAGCGCGCGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
DB 1 GCGCCAGCGCGCAGCGCGCGCGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
QY 61 CCGGAGCTCAACATCGCTGCTCGCGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTC 120
DB 61 CCGGAGCTCAACATCGCTGCTCGCGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTC 120
QY 121 CTGCGAGTGTCTTCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 CTGCGAGTGTCTTCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 TACAATCCCTTGGAGAGCG 240
DB 181 TACAATCCCTTGGAGAGCG 240
QY 241 CTGAGCCTCTCTCAGATCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 CTGAGCCTCTCTCAGATCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 TGGCTGCAATGTCTTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 301 TGGCTGCAATGTCTTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 GTGAGACTGTCTGTTTCCAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB 361 GTGAGACTGTCTGTTTCCAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 421 AGTGTGTGATGAGCGCGCTTTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 421 AGTGTGTGATGAGCGCGCTTTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

QY 481 CATTGCGAGTACCTGCTCCAGGCAATATTCAAGAGTTCTGCTACATCATGATACGCTGG 540
Db 481 CATTGCGAGTACCTGCTCCAGGCAATATTCAAGAGTTCTGCTACATCATGATACGCTGG 540
QY 541 TTTTCCCTTTGANTGTCAGCACTGCAAACTGAAGTTTGGGTCCTGCTTACGAGGCTGG 600
Db 541 TTTTCCCTTTGANTGTCAGCACTGCAAACTGAAGTTTGGGTCCTGCTTACGAGGCTGG 600
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Db 601 TCCTTGAGTCTGAGATGAGGAGGAGATATCAGTGGCTATATCCCAATGAGATGG 660
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Db 661 GACTAGTGGCAATCCCGGCAAGAGAGAGTGAAGTTTCTATGAGTCTGCTCAAGAGCCC 720
QY 721 TACCCGAGTACCTTTCAAGTGAACATGCGCGGAGGAGCGCTCTACTATGAGCTCAAC 780
Db 721 TACCCGAGTACCTTTCAAGTGAACATGCGCGGAGGAGCGCTCTACTATGAGCTCAAC 780
QY 781 CTGCTGATCCCTGCTGCTCATCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 840
Db 781 CTGCTGATCCCTGCTGCTCATCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 840
QY 841 GATTCCGGGAGAGATTTCCCTGGGATTAACAGTCTTACTCTCTCTTACCGTCTTCATG 900
Db 841 GATTCCGGGAGAGATTTCCCTGGGATTAACAGTCTTACTCTCTCTTACCGTCTTCATG 900
QY 901 CTGCTGCTGCTGAGATCATGCTCGGCTCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
Db 901 CTGCTGCTGCTGAGATCATGCTCGGCTCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
QY 961 TTCCGCGAGCACCATGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 961 TTCCGCGAGCACCATGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1021 TACCACCAACGACCGGCGGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1080
Db 1021 TACCACCAACGACCGGCGGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1080
QY 1081 AACTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 AACTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
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Db 1201 CCGCCCGGAGCAACGCGGAACTGCTGTAATGCGGCTTCCGCGGCTGGAAGGCTGGAC 1260
QY 1261 TGTGTCGCGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
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Db 1321 GATGAGCACTTCTGCAACGCGGAGCAACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
QY 1381 CTGAGGAGGCTCGGCTGTAATGCGGCTTCCGCTGCGGAGGAGGAGGAGGAGGAGGAGG 1440
Db 1381 CTGAGGAGGCTCGGCTGTAATGCGGCTTCCGCTGCGGAGGAGGAGGAGGAGGAGGAGG 1440
QY 1441 TCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
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QY 1501 GTCTTCAACCATCATCTGCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
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QY 1561 GTGTCCAAAGACTTTTGGTAAACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620

Db 1561 GTGTCCAAAGACTTTTGGTAAACGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
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QY 1681 AACTCCAGTGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 AACTCCAGTGTTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1741 GTAGTAGAATCTCAGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Db 1741 GTAGTAGAATCTCAGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
QY 1801 CATCCGTACCATCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
Db 1801 CATCCGTACCATCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
QY 1861 TGAAGAGGCTTCCGGA 1876
Db 1861 TGAAGAGGCTTCCGGA 1876

RESULT 8

US-08-771-737-1
; Sequence 1, Application US/08771737
; Patent No. 6323000
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/08/771,737
; CURRENT FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)...(1514)
US-08-771-737-1

Query Match 82.2%; Score 1543; DB 4; Length 1590;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1555; Conservative 1; Mismatches 21; Indels 0; Gaps 0;
QY 72 CATGGCTGCTGCGCGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131
Db 8 CATGAGGTGTAGCCCGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 67
QY 132 CCTGCNAGGCGGAGTTCAGAGGAGGAGTTCAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTG 191
Db 68 CCTGCNAGGCGGAGTTCAGAGGAGGAGTTCAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTG 127
QY 192 GGAGAGGCGGCTGGGCAATGACTCGCAACCACTACCGCTTACTTCTGCTGCTGCTGCTGCT 251
Db 128 GGAGAGGCGGCTGGGCAATGACTCGCAACCACTACCGCTTACTTCTGCTGCTGCTGCTGCT 187
QY 252 GCAGATCATGAGCTGGATGAGAGAACCAAGTTTAAACCAACCAATTTGGCTGCAAT 311
Db 188 GCAGATCATGAGCTGGATGAGAGAACCAAGTTTAAACCAACCAATTTGGCTGCAAT 247

312 GTCTTGGACAGATCACTATTTTACAGTGAATGTGAGAAATATCCAGGGGTGAAGACTGT 371
Db
248 GTCTTGGACAGATCACTATTTTACAGTGAATGTGAGAAATATCCAGGGGTGAAGACTGT 307
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372 TCGTTTCCAGATGCGCAGATTGGAAACCCAGACATTCCTCTATAACAGTGTGATGA 431
Db
308 TCGTTTCCAGATGCGCAGATTGGAAACCCAGACATTCCTCTATAACAGTGTGATGA 367
Qy
432 GCGCTTTGACGCGACATNTCCACACTAACTGTTGGTGAATTCCTGGGCATTGGCCAGTA 491
Db
368 GCGCTTTGACGCGACATNTCCACACTAACTGTTGGTGAATTCCTGGGCATTGGCCAGTA 427
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492 CCGTCTCCAGGCAATATCAAGAGTTCTCTGCTACATGATGATGATGATGATGATGATGAT 551
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428 CCGTCTCCAGGCAATATCAAGAGTTCTCTGCTACATGATGATGATGATGATGATGATGAT 487
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552 TGTGAGCACTGCAAACTGAAAGTTTGGGTCTGCTGCTTACGAGAGGTGCTCTTGGATCT 611
Db
488 TGTGAGCACTGCAAACTGAAAGTTTGGGTCTGCTGCTTACGAGAGGTGCTCTTGGATCT 547
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612 CGAGATGCGAGGAGGAGATATCAGTGGCTATATCCCAATGAGATGAGATGAGATGAGTGG 671
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548 CGAGATGCGAGGAGGAGATATCAGTGGCTATATCCCAATGAGATGAGATGAGATGAGTGG 607
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672 AATCCCGGCAAGAGAGGTGAAAGTTTCTATGAGTCTGCAAGAGCCCTACCCCGATGT 731
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668 CACCTTACAGTACCATGCGCGAGAGGCTCTACTATGAGTCTGCAAGAGCCCTACCCCGAT 727
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792 CTGTGTGCTCATCTCCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db
728 CTGTGTGCTCATCTCCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
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852 GAAGATTTCCTCGGGGATTAACAGTCTTACTCTCTTTACCGTCTTCTATGCTGCTGCTGCT 911
Db
788 GAAGATTTCCTCGGGGATTAACAGTCTTACTCTCTTTACCGTCTTCTATGCTGCTGCTGCT 847
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912 TGAGATCATGCTCGGCAACATCCGATTCGGTACCATGATGATGATGATGATGATGATGATGAT 971
Db
848 TGAGATCATGCTCGGCAACATCCGATTCGGTACCATGATGATGATGATGATGATGATGATGAT 907
Qy
972 CATGATCATGCTGGGCTCTCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1031
Db
908 CATGATCATGCTGGGCTCTCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 967
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1032 CGACCCCGACGGGGGCAAGATGCCCAAGTGGACAGAGTCACTCTTCTGAACTGGTGGC 1091
Db
968 CGACCCCGACGGGGGCAAGATGCCCAAGTGGACAGAGTCACTCTTCTGAACTGGTGGC 1027
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1092 GTGGTTCTCGAATGAAGAGCCCGGGGAGGACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1151
Db
1028 GTGGTTCTCGAATGAAGAGCCCGGGGAGGACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1087
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1152 GCAGCGGCTGCGAGCTGCGCAGTGTGGATGAGCGCGCTGGCGCGCGCGCGCGCGCGCG 1211
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1088 GCAGCGGCTGCGAGCTGCGCAGTGTGGATGAGCGCGCTGGCGCGCGCGCGCGCGCGCG 1147
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1212 CAACGGGAACCTGTGTACATCGGCTTCCGCGGCTTCCGAGCGGTGACATGCTGTGCTGGAC 1271
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1148 CAACGGGAACCTGTGTACATCGGCTTCCGCGGCTTCCGAGCGGTGACATGCTGTGCTGGAC 1207
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1272 CCGGACTCTGGGGTAGTGTGCGCGCATGGCTGCTCCCGGCGCGCGCGCGCGCGCGCGCG 1331
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1208 CCGGACTCTGGGGTAGTGTGCGCGCATGGCTGCTCCCGGCGCGCGCGCGCGCGCGCGCG 1267
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1332 CCGGACTCTGGGGTAGTGTGCGCGCATGGCTGCTCCCGGCGCGCGCGCGCGCGCGCGCG 1391
Db
1268 CCGGACTCTGGGGTAGTGTGCGCGCATGGCTGCTCCCGGCGCGCGCGCGCGCGCGCGCG 1327
Qy
1392 CCGGACTCTGGGGTAGTGTGCGCGCATGGCTGCTCCCGGCGCGCGCGCGCGCGCGCGCG 1451

1328 CCGCTACATTCGCAACCGCTTCCGCTGCCAGGACGAAAGCGAGGCGGTCTGCAGGAGTG 1387
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1452 GAAGTTCCGCGCTGTGTGGTGGACCGCTGTGCTCATGGCTTCTCGGTCTTCCACCAT 1511
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1388 GAAGTTCCGCGCTGTGTGGTGGACCGCTGTGCTCATGGCTTCTCGGTCTTCCACCAT 1447
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1512 CATCTGCACCATCGGCATCTGATGCTCGGCTCCCAACTTCTGTGGAGGCGGTCTCCAAAGA 1571
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1448 CATCTGCACCATCGGCATCTGATGCTCGGCTCCCAACTTCTGTGGAGGCGGTCTCCAAAGA 1507
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1572 CTTTCGCTAAACACCGCTGCTGTATGATGTGGAATACTCACATGGGCGAGGCTTT 1631
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1508 CTTTCGCTAAACACCGCTGCTGTATGATGTGGAATACTCACATGGGCGAGGCTTT 1567
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1632 GCGTTGGCGAGATTGG 1648
Db
1568 GCGTTGGCGAGATTGG 1584

RESULT 9
US-09-954-936-1
; Sequence 1, Application US/09954936
; Patent No. 6683157
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017. US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)...(1514)
US-09-954-936-1

Query Match 82.2%; Score 1543; DB 4; Length 1590;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1555; Conservative 1; Mismatches 21; Indels 0; Gaps 0;

Qy 72 CATGCGTGTCTCGCGGAGGCGCTGTGCTGGCGGTGGCGCGCTCGCTCGCTCGACGTC 131
Db 8 CATGAGGTGTAGCCCCCGGAGGAGTGTGGCTGGCACTGGCAGCATCTCTCTCGACGTC 67
Qy 132 CTTGCAAGGCGAGTTCAGAGGAGGCTTTTACAGGAGCTGTGTCAAGAACTACATCCCTT 191
Db 68 CTTGCAAGGCGAGTTCAGAGGAGGCTTTTACAGGAGCTGTGTCAAGAACTACATCCCTT 127
Qy 192 GGAAGAGCCCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCTAGGCGTCT 251
Db 128 GGAAGAGCCCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCTAGGCGTCT 187
Qy 128 GGAAGAGCCCGTGGCCAAATGACTCGCAACCACTCACCGTCTACTTCTCTAGGCGTCT 187
Qy 252 GCAGATCATGGAAGTGTGATGAGAGAACCAAGTTTAAACCAATTTGGTGGCAAT 311
Db 188 GCAGATCATGGAAGTGTGATGAGAGAACCAAGTTTAAACCAATTTGGTGGCAAT 247
Qy 312 GTCTTGAACAGATCACTATTATAGTGGATGTGAGATATCCAGGGGTGAAGACTGT 371

Db 248 GTCTTGACAGATCACTATTTCAGTGGATGTGTCAGATATCCAGGGGTGAAGACTGT 307
QY 372 TCGTTTCCAGATGGCGAGATTGGAAAACAGACATTTCTCTATTAACAGTCTCTATGA 431
Db 308 TCGTTTCCAGATGGCGAGATTGGAAAACAGACATTTCTCTATTAACAGTCTCTATGA 367
QY 432 GCGCTTTGAGCGGCACATTCACACATCAAGTGTGGTGAATTTCTTGGGCAATTCGCCAGTA 491
Db 368 GCGCTTTGAGCGGCACATTCACACATCAAGTGTGGTGAATTTCTTGGGCAATTCGCCAGTA 427
QY 492 CTTGCGCTCCAGGCATATTCAGAGTTCCTCTCATATCATCATGATGATGCTGGTTTCCCTTTGA 551
Db 428 CTTGCGCTCCAGGCATATTCAGAGTTCCTCTCATATCATCATGATGATGCTGGTTTCCCTTTGA 487
QY 552 TGTGAGCACTGCAAACTGAATTTGGTGTCTGTGCTTACGAGGCTGTGCTCTGATCT 611
Db 488 TGTGAGCACTGCAAACTGAATTTGGTGTCTGTGCTTACGAGGCTGTGCTCTGATCT 547
QY 612 GCAGATCAGAGGACAGATATCACTGTGCTATATCCCAATGGAGAATGGGACCTAGTGGG 671
Db 548 GCAGATCAGAGGACAGATATCACTGTGCTATATCCCAATGGAGAATGGGACCTAGTGGG 607
QY 672 AATCCCCGCGAAGAGGAGTGAAGGTTCTATGATGCTGCAAAAGAGCCCTACCCCGATGT 731
Db 608 AATCCCCGCGAAGAGGAGTGAAGGTTCTATGATGCTGCAAAAGAGCCCTACCCCGATGT 667
QY 732 CACCTTACAGTACCATGCGCCGAGGAGCTCTACTATGGCTCAACCTGATGATCCC 791
Db 668 CACCTTACAGTACCATGCGCCGAGGAGCTCTACTATGGCTCAACCTGATGATCCC 727
QY 792 CTGTGTGCTCATCTCCGCGCTCGCCCTGCTGTGTTCTCTGCTGAGATTCGGGGA 851
Db 728 CTGTGTGCTCATCTCCGCGCTCGCCCTGCTGTGTTCTCTGCTGAGATTCGGGGA 787
QY 852 GAAATTTCTCGGGATTAACAGTCTTACTCTCTTACCGTCTTCTGCTGCTGCTGCTG 911
Db 788 GAAATTTCTCGGGATTAACAGTCTTACTCTCTTACCGTCTTCTGCTGCTGCTGCTG 847
QY 912 TGAGATCATGCGGCAACATCCGATTCGCTGATGATGATGATGATGATGATGATGATG 971
Db 848 TGAGATCATGCGGCAACATCCGATTCGCTGATGATGATGATGATGATGATGATGATG 907
QY 972 CATGATCATGCTGGGCTCTCGGTGTGTGATGATGATGATGATGATGATGATGATGATG 1031
Db 908 CATGATCATGCTGGGCTCTCGGTGTGTGATGATGATGATGATGATGATGATGATGATG 967
QY 1032 CGACCCGAGCGGGGAGATGCCAAGTGGACACAGATCATCTTCTGAACTGTGCTGCGC 1091
Db 968 CGACCCGAGCGGGGAGATGCCAAGTGGACACAGATCATCTTCTGAACTGTGCTGCGC 1027
QY 1092 GTGGTTCTCTSCGAATGAAGAGCCCGGGGAGACAGAGTGGCGCGGCTGCGCAGCAAA 1151
Db 1028 GTGGTTCTCTSCGAATGAAGAGCCCGGGGAGACAGAGTGGCGCGGCTGCGCAGCAAA 1087
QY 1152 GCAGCGGCGCTGAGCTGCGCAGTGTGGAGATGAGCGCGTGGCGCGCGCGCGCGCAG 1211
Db 1088 GCAGCGGCGCTGAGCTGCGCAGTGTGGAGATGAGCGCGTGGCGCGCGCGCGCGCAG 1147
QY 1212 CAAAGGGAACCTGCTGATCATGCTGCTGCGCGCTGAGAGGCGGTGCTGCTGCTGCTG 1271
Db 1148 CAAAGGGAACCTGCTGATCATGCTGCTGCGCGCTGAGAGGCGGTGCTGCTGCTGCTG 1207
QY 1272 CCGCGACTCTGGGCTAGTGTGCGCGCATGCGCTGCTGCGCGCATGCGCGCATGCGCG 1331
Db 1208 CCGCGACTCTGGGCTAGTGTGCGCGCATGCGCTGCTGCGCGCATGCGCGCATGCGCG 1267
QY 1332 CTTGCAAGCGGGCAACCCCGGAGGAGGAGCCCGGAGCTTGGCCAAAGATCTTGAGAGGT 1391
Db 1268 CTTGCAAGCGGGCAACCCCGGAGGAGGAGCCCGGAGCTTGGCCAAAGATCTTGAGAGGT 1327
QY 1392 CCGCTATATTGCCAATGCTCTCGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1451
Db 1328 CCGCTATATTGCCAATGCTCTCGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1387

QY 1452 GAAGTTGCGCGCTGTGTGTGGACCGCCTGTGCTCTCATGGCCTTCTCGTCTTCAACCAT 1511
Db 1388 GAAGTTGCGCGCTGTGTGTGGACCGCCTGTGCTCTCATGGCCTTCTCGTCTTCAACCAT 1447
QY 1512 CATGTGACATCGGCATCCTGATGTGCGCTCCCACTTCTGTTGAGGCGGTGTTCCAAAGA 1571
Db 1448 CATGTGACATCGGCATCCTGATGTGCGCTCCCACTTCTGTTGAGGCGGTGTTCCAAAGA 1507
QY 1572 CTTTGGTGAACACGCTGCTGTTCTGTACATGTGGAACCTCACAGATGGGCAAGGCTTT 1631
Db 1508 CTTTGGTGAACACGCTGCTGTTCTGTACATGTGGAACCTCACAGATGGGCAAGGCTTT 1567
QY 1632 GGCTTGGCGAGATTG 1648
Db 1568 GGCTTGGCGAGATTG 1584

RESULT 10
US-08-496-855A-1
; Sequence 1, Application US/08496855A
; Patent No. 5801232
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,855A
; FILING DATE: 20-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9369B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 166..1755
; US-08-496-855A-1

Query Match 19.3%; Score 362.2; DB 1; Length 2277;
Best Local Similarity 54.4%; Pred. No. 1.6e-79;
Matches 780; Conservative 0; Mismatches 643; Indels 12; Gaps 2;

110 CCGGCTCGCTCTCTGACGCTGCTCCGCAAGCGGAGTTCCAGAGGAAGCTTTACAGGAGC 169
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302 CCACGGGATTCGCGAGGAGGCTCGCATACCGAGACTGAGGACGGCTCTTCAAACACC 361
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170 TGGTCAAGAACTACAATCCCTTGGAGAGGCGCGTGGCCCAATGACTCGCAACCACTCACCG 229
Db
362 TCTTCGCGGGCTACAACCGCTGGGCGCGCGCTGGCCCAACCTTTCAGACGCTGGTGTG 421
Qy
230 TCTACTTCTCCTCGAGCTCTCGAGATCATGGAGCTGAGAGGAGGAGCAAGTTTAA 289
Db
422 TGGCTTTGGACTGTCCATCGCTCAGCTCATGATGTGATGAGAGCAACCAATGATGA 481
Qy
290 CCACCAACATTTGGCTGCAATGTCTTGGACAGATCACTATTTACAGTGGAAATGTGTGAG 349
Db
482 CCACCAAGCTCTGGCTAAACAGGAGTGGAGCGACTACAACCTGGCTGGAAACCCCGCTG 541
Qy
350 AATATCCAGGGGTGAAGACTGTTCTGTTTCCAGATGGCCAGATTTGGAAACAGACATTC 409
Db
542 AATTTGGCAACATCACATCTCTCAGGGTCCCTTCTGAGATGATCTGGATCCCGACATTC 601
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410 TTCTCTATAACAGTGTCTGATGAGCGCTTTGAGCGCCACATTCACACTAACGTTGTGTGA 469
Db
602 TTCTCTACAAATGACAGATGGGAGTTTGCAGTGACCAATGACCAAGGCCCACTCT 661
Qy
470 ATTCTTTGGCAATGCCAGTACCTGCTCCAGGCAATTTCAAGAGTTTCTGCTACATCG 529
Db
662 TCTCACGGGCACTGTGACCTGGGTGCCCCCGGCCATCTACAAGAGCTCTCTGCAGCATCG 721
Qy
530 ATGTACGCTGTTTCCCTTTGATGTGAGCACTGCAAACTGAAGTTTGGTCTGTTT 589
Db
722 AGCTCACCTTCTTCCCTTTGACCAAGCAAGTGAAGATGAAGTTTGGCTCTGGATTT 781
Qy
590 ACGGAGGCTGGCTTGTGATCTGACATGTCAGGAG-----GCAGATATCACTGCTATA 643
Db
782 ATGCAAGGCCAAGATGACCTTGGAGCAGATGAGACAGACTGTGACCTGAAGACTACT 841
Qy
644 TCCCAATGGAATGGAATCTAGTGGAAATCCCGCAAGAGGAGTGAAGTTTCTATG 703
Db
842 GGGAGCGGCGAGTGGGCGCATCGTCAATGCCACGGCGACCTTACAACAGCAAGAGTACG 901
Qy
704 AGTGTGCAAGAGGCGCTTACCGGATGTCACCTTACAGTGACCATGCGCGCAGAGCG 763
Db
902 ACTGTGCGCGAGATCTACCGGAGCTCACCTACGCTTGTGATCGCGGCGGCTGCGCG 961
Qy
764 TCTACTATGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCGCTCTGCGCTGCTGG 823
Db
962 TCTTTACACCACTCAACCTCATCTCCTGCTGCTCATCTCTCTGCTCATCTGCTGCTGG 1021
Qy
824 TGTTCCTGCTTCTGAGATTCGGGGAGAAATTTCCCTGGGATTAACAGTCTTACTCT 883
Db
1022 TCTTCTACCTGCTCCGACTCGGCGAGAGATCACGCTGTGCAATTTGCTGCTGCTGT 1081
Qy
884 CTCTTACCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
Db
1082 CACTCACCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1141
Qy
944 CATTTAGTACCCAGTACTTTCGCGAGCACCATGATCATCTGCGGCTCTCGTGGTGTGA 1003
Db
1142 CGCTCATCGCGAGTACTGCTGTTTCAACATGATCTTCTGCTCACCTGCTCATCATCA 1201
Qy
1004 CGGTGATGCTGTGAGTACACCAACAGACCGCGAGGCGGAGAGTGGCCCAAGTGA 1063
Db
1202 CGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1261
Qy
1064 CCAGAGTATCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
Db
1262 TGGCGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321
Qy
1124 ACAAGTGGCGCGGCTGCGACCAAGAGCGGCGCTGCGAGCTTGGCGAGTGTGAGA 1183
Db
1322 CGGTGAGTCTGCGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1381
Qy
1184 TGAGCGCGGCG 1243

Db 1382 GCAACGTGGATGCGCGAGGAGGAGGAGTGGTGGTGGAGGAGGAGACAGATGGGCTGTG 1441
Qy 1244 GCCTGGAGGGGTGCTACTGTGTCCGACCCCGGACTCTGGGGTGTGTGTGGCCGCTAGG 1303
Db 1442 CAGGTCTATGTGGCCCCCTCTGTGGGACCCCTCTGCGAGGAGGAGGAGGAGGAGG 1501
Qy 1304 CCTGCTCCCCCAGCAGCAGTATGAGCAGCTCTCTGCGAGGCGGCGGAAACCCCGGAGG 1363
Db 1502 CTTGAGGTCCCAAGGCTGAGGCTCTGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 1555
Qy 1364 CGGACTTGGCCCAAGATCTGAGGAGGAGTCCGCTACATTTGCCAATGCTTCCGCTGCCAG 1423
Db 1556 CCCACATGCGAGAGGAGGAGTGGAGGAGTGTGCACTACTGCGGAGGAGGAGGAGGAG 1615
Qy 1424 ACGAAAGCGGAGGCGGTCTGCGAGGAGTGAAGTTTGGCGGCGCTGTGTGTGGAGCGGCTGT 1483
Db 1616 ATGTGACTTTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1675
Qy 1484 GCCTCATGGCTTCTCGGCTTTCACCATCATCTGCAACCATCGGAGGAGGAGGAGGAG 1538
Db 1676 TCCCTGCTGCTTATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1730

RESULT 11
US-08-487-596-1
; Sequence 1, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESS: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 166..1755
OTHER INFORMATION: /product= "ALPHA-2 SUBUNIT"
US-08-487-596-1

Query Match
Best Local Similarity 54.4%; Pred. No. 1.6e-79;
Matches 780; Conservative 0; Mismatches 643; Indels 12; Gaps 2;

110 CCGGCTCGCTCCCTGACGCTGCTCCGCAAGCGGAGTTCCAGAGGAAGCTTTACAAGGAGC 169
Db 302 CCAGGGATGTCGCGCAGGGAGGCTCGATACCGAGACTGAGGACCGGCTCTTCAAACACC 361
Qy 170 TGGTCAAGAACTACAATCCCTTGGAGAGCGCGTGGCCAAATGACTCGCAACCACTCACCG 229
Db 362 TCTTCCGGGGCTACAACCGCTGGCGCGCGCGTGGCCAACTTCAAGAGCTGGTATTG 421
Qy 230 TCTACTTCTCCCTGAGGCTCTCGAGATCATGGAGCTGGATGAGAGAACCAAGTTTAA 289
Db 422 TGGCTTTTGGACTCTCCATGCTCAGCTCATGATGAGTGGATGAGAGAACCAAGTATGA 481
Qy 290 CCACCAACATTTGGCTGCAATGCTTGGACAGATCACTATTACAGTGGAAATGTGCAG 349
Db 482 CCACCAACGCTGGCTAAACAGAGTGGAGCGACTCAAACTGGCTGGAAACCCGCTG 541
Qy 350 AATATCCAGGGGTGAAGACTGTTGTTTCCAGATGGCCGATTTGGAAACCAAGATTC 409
Db 542 ATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGAGATGATCTGGATCCCGACATTG 601
Qy 410 TTTCTATAACAGTCTGATGAGCGCTTTGAGCGCCACATTCCACACTAACGTTGTGGA 469
Db 602 TTCTCTACAACATGCAATGGAGTTTGGAGTGACCCACATGACCAAGGCCACCTCT 661
Qy 470 ATTCTTGGGCAATGGCAGTACCTGCTCCAGGCATATTCAGAGATTCCTGCTACATCG 529
Db 662 TCTCCAGGGCACTGTGACTGGGTGCCCCGGCCATCTACAAGACTCCTGCGAGCTCG 721
Qy 530 ATGTACGCTGTTTCCCTTTGATGTCAGACTGCAAACTGAAGTTGGGTCTGCTGCTT 589
Db 722 ACCTCACCTTCTTCCCTTCCAGCAGCACTGCAAGATGAAGTTGGCTCCTGGACTT 781
Qy 590 ACGGAGGCTGGTCTTGGATCTGACAGATGACAGGAG-----GCAGATATCAGTGGCTATA 643
Db 782 ATGCAAGGCCAAGATCGACTTGGAGAGATGAGAGCACTGTGACCTGAGGACTACT 841
Qy 644 TCCCCAATGGAGATGGGACCTAGTGGGAATCCCCGGCAAGAGGAGTGAAGTTCTATG 703
Db 842 GGGAGAGCGCGAGTGGGCGCATCGTCAATGCGCACCGGCACTTACACAGCAAGAGTACG 901
Qy 704 AGTGTGCAAGAGCGCTTACCGGATGTCACCTTACAGTGACCATGCGCCGAGGAGCGC 763
Db 902 ACTGTGCGCCGAGATCTACCCGAGCTCACCTACGCTTCTGTCATCCGGCGGCTGCGCG 961
Qy 764 TCTACTATGGCTCAACCTGCTGATCCCGTGTGCTCATCTCCGCGCTCGCCCTGCTGG 823
Db 962 TCTTCTACACCATCAACCTCATATCCCTGCTGCTCATCTCTGCTGCTGCTGCTGCTGCTG 1021
Qy 824 TGTTCCTGCTCTCTGAGATTCGCGGAGAAAGATTTCCCTGGGGATTAACAGTCTTACTCT 883
Db 1022 TTTTCTACTGCTCCCTCGACTCGGCGAGAGATCATCGCTGTGCAATTTGGTGTGCTGT 1081
Qy 884 CTCCTTACCGTTCATGCTGCTGGCTGAGATCATGCGCGGCAACATCCGATTCGGTAC 943
Db 1082 CACTCACCGCTTCTCTGCTGCTCATCACTGAGATCATCCCGTCCACCTCGCTGGTCACTCC 1141

944 CATTGATAGCCAGTACTTTCGCGAGCACCATGATCATCTGGGCGCTTCTCGGTGGTGTGA 1003
Db 1142 CGCTCATCGCGAGTACTGCTGTTTCCATGATCTTCGTACCCCTGTCCATGTCATCA 1201
Qy 1004 CGGTGATCGTGTGAGTACCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1063
Db 1202 CGGTCTTCTGCTCAATGTGCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1261
Qy 1064 CCAGAGTCACTCTTCTGAAGTGTGCGGTGCTCTCGAATGAAGAGAGAGAGAGAGAG 1123
Db 1262 TCGCGGGGGCGCTTCTGCGGTGCTGCTGCGGTGCTGCTGCGGTGCTGCTGCGGTGCT 1321
Qy 1124 ACAAGGTGCGCGCGCTTCCAGCAACAAGCAGCGCGCTGCGAGCTTGGCCCTGAGTGTG 1183
Db 1322 CGGTGAGCTCTGCCACCCCTAGGCTGAAGCTCAGCCCTCTTATCACTGGCTGAGAG 1381
Qy 1184 TGAGCGCGGTGGCG 1243
Db 1382 GCAACCTGGATGCGGAG 1441
Qy 1244 GCCTGGAGCGGTGCTGCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1303
Db 1442 CAGGTGATGCGCGCGCTTCTGCGGTGCTGCGGTGCTGCGGTGCTGCGGTGCTGCGGT 1501
Qy 1304 CTTGCTCCCCCAAGCAGTACCTCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1363
Db 1502 CCTCAGGTGCGCGCGCTGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1555
Qy 1364 CGGACTTGGCGCAAGATCTGCGAGAGAGTCCGCTACATTCGCTGCTGCTGCTGCTG 1423
Db 1556 CCCACATGCAAGAGGCACTGGAAGGTGTCATGCTGCGCGCGCGCGCGCGCGCGCG 1615
Qy 1424 ACAGAAACGAGGCGGTCTGCGAGCGAGTGAAGTTCGCGCGCTGCTGCTGCTGCTG 1483
Db 1616 ATGCTGACTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1675
Qy 1484 GCCTGATGCGCTTCTGCTGCTTCCATCATCATTCACCATTCGACCATCGGATCTCT 1538
Db 1676 TCCTCTGCTGCTTATCATGCTGCTTCTGCGGAGCACTCGGCTCTTCTGCTGCT 1730

RESULT 12
US-08-660-451A-1
; Sequence 1, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Hallier & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 06/07/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0082

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 555...2141
OTHER INFORMATION: alpha2 subunit of human neuronal
OTHER INFORMATION: nicotinic acetylcholine receptor
NAME/KEY: 5'UTR
LOCATION: 1...554
OTHER INFORMATION:
NAME/KEY: 3'UTR
LOCATION: 2142...2666
OTHER INFORMATION:
US-08-660-451A-1

Query Match 19.3%; Score 362.2; DB 4; Length 2664;

Best Local Similarity 54.4%; Pred. No. 1.7e-79;

Matches 780; Conservative 0; Mismatches 643; Indels 12; Gaps 2;

QY	110	CGCGTCTGCTCTGCAAGTGTCCCTGCAAGGGAGTTCAGAGGAGCTTTACAAAGGAGC	169
DB	691	CAACGGCATTCGCGCAGGAGGCTCGCATACGAGACTGAGACCGGCTCTTCAACACC	750
QY	170	TGGTCAAGAACTACAAATCCCTTGGAGAGCCCGTGGCCAAATGACTCGCAACCACTCACCG	229
DB	751	TCTTCGGGGCTACAAACCGCTGGCGCGCGGTGCCCAACACTTCAGACGTGGTATTG	810
QY	230	TCTACTTCTCCGTAGCCCTCTGAGATCATGAGATGAGATGAGAGCAAGCAAGTTTAA	289
DB	811	TGCGCTTTGGAGTGTCCATCGCTCAGCTCATCGATGTGATGAGAGAAACCAATGATGA	870
QY	290	CCACCAACATTTGGCTGCAAAATGTCTTGACAGATCACTATTACAGTGGAAATGTGTGAG	349
DB	871	CCACCAACGTCTGGCTTAAACAGAGAGTGGAGCGACTACAACTGCGTGGAAACCCGCTG	930
QY	350	AATATCCAGGGGTGAAGACTGTTCGTTCCAGATGGCCAGATTTGGAAACAGACATTC	409
DB	931	ATTTTGGCAACATCATCTCTCAGGGTCCCTTCTGAGATGATCTGGATCCCGGACATTG	990
QY	410	TTCTCTATACAGTCTGATGAGCGTTTGAGCCACATTCACACTAACGTGTGGTGA	469
DB	991	TTCTCTACAAATGAGATGGGAGTTTGCAGTGACCCACATGACCAAGGCCCACTCT	1050
QY	470	ATTCTTCTGGCATTCGCCAGTACCTGCTCCAGGCAATATTCAAGAGTTCTCTGCTACATCG	529
DB	1051	TCTCCAGGGGCACTGTGCACTGGGTGCCCGGCCATCTACAGAGCTCTCTGAGCATCG	1110
QY	530	ATGTAGCGTGGTTCCCTTTGATGTGACAGACTGCAAACTGAAATTTGGGTCTGTGCTTT	589
DB	1111	AGTCACTCTTCTCCCTTCGACCAAGAGAGTGTGCAAGATGAATTTGGCTCTCGGACTT	1170
QY	590	ACGGAGCTGGTCTTGGATCTGCAGATCGCAACTGCAAGTGGGCTATG	643
DB	1171	ATGACAAGGCCAAGATCGACCTGGAGCAGATGGAGCAGACTGTGGACCTGAAGGACTCT	1230
QY	644	TCCCCAATGAGAAATGGGACCTAGTGGGAATCCCGGCAAGAGAGTGAAGATTTCTATG	703
DB	1231	GGGAGAGCGGAGTGGGCCATCTCAATGCCACGGGACCTTACACAGCAAGAGTACG	1290

QY	704	AGTCTGCAAGAGAGCCCTACCCGATGTCACTTACAGTAGCAATCGCGCAGGAGCGC	763
DB	1291	ACTGCTGCGCGAGATCTACCCCGAGCTCACTACGCTTGTGTCATCGCGGCTCGCGC	1350
QY	764	TCTACTATGGCTCAACTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTG	823
DB	1351	TCTTACACATCAACCTCATATCCCTGCTGCTCATCTCTGCTCATCTGCTGCTG	1410
QY	824	TGTTCTGCTTCTCTGAGATTCGCGGGAGAAATTTCCCTGGGGATAACAGTCTTACTCT	883
DB	1411	TCTTCTACTGCTTCTGAGCTGCGCGGAGAGATCACTGCTGCTATGCTGCTGCTG	1470
QY	884	CTTTTACCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	943
DB	1471	CACTCACCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1530
QY	944	CATTGATAGCCAGTACTTCGCGAGCACCATGATGATGCTGCTGCTGCTGCTGCTG	1003
DB	1531	CGCTCATCGCGGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1590
QY	1004	CGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1063
DB	1591	CGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1650
QY	1064	CCAGAGTCACTCTTCTGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1123
DB	1651	TGCGGGGGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1710
QY	1124	ACNAGGTGCGCCCGCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1183
DB	1711	CCGTGGAGCTCTGCCACCCCTACGCCCTGAAAGCTCAGCCCTCTTATCATCTGCTG	1770
QY	1184	TGAGCGCGTGGCG	1243
DB	1771	GCAAGTGGATGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1830
QY	1244	GCCTGGAGCGGTGCACTGTGTCCGACCCCGGACTCTGGGGTAGTGTGTGGCGCATGG	1303
DB	1831	CAGGTCACTGTGGCG	1890
QY	1304	CCTGCTCCCGCAGCAGCATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1363
DB	1891	CCTCAGGTCCCAAGGCTGAGGCTGTGCTGCGAGGAGGAGGAGGAGGAGGAGGAGG	1944
QY	1364	CGGACTTGGCCCAAGATCTCTGAGGAGGTCCTGCTACATTTGCCAATCGTTCCGCTG	1423
DB	1945	CCCATGCGAAGAGGCACTGCAAGGTGTCACTACATTTGCCGACCCACCTGCGGTCTG	2004
QY	1424	ACGAAAGCGAGCGGTCTGCGAGGAGTGGAAATTCGCGCGCTGTGTGTGGTGGACCG	1483
DB	2005	ATGCTGACTCTTCGGTGAAGGAGGACTGGAAGTATGTTGCCATGCTCATCGAGATCT	2064
QY	1484	GCTCATGCGCTTCTCGGTCTTCAACCATCATCTGCAACCATCGGCATCTGATGTC	1538
DB	2065	TCTCTGCTGTTTATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2119

RESULT 13

US-08-466-589-1

Sequence 1, Application US/08466589

Patent No. 5837489

GENERAL INFORMATION:

APPLICANT: Eliot, Kathryn J.

APPLICANT: Ellis, Steven B.

APPLICANT: Harpold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

NUMBER OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Brown, Martin, Haller & McClaim

STREET: 1660 Union Street

CITY: San Diego

STATE: CA
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,589
 FILING DATE: June 5, 1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: March 8, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-9950
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-238-0999
 TELEFAX: 619-238-0062
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2068 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 166..1752
 US-08-466-589-1

Query Match 18.4%; Score 345.8; DB 2; Length 2068;
 Best Local Similarity 54.1%; Pred. No. 1.6e-75;
 Matches 776; Conservative 0; Mismatches 644; Indels 15; Gaps 3;

110 CCGGCTCGCTCTCCAGCTGTCCTGCAAGCGCGAGTTCACGAGGAAGCTTTACAGGAGC 169
 302 CCACGGCATTCGCCGAGGAGCTCGATACCGAGAGTGGAGCGGCTCTTCAACACC 361
 170 TGGTCAAGAACTACAACTCCCTTGGAGAGGCGCGTGGCGAATGACTCGCAACCTACCG 229
 362 TCTTCCGGGGCTACAAACGCTGGGCGCGCGGTCGCCAATCTTACAGCTGTGATG 421
 230 TCTACTTCTCCTGAGCCTCTCGAGATCATGGAGCTGATGAGAGCAACCAAGTTTAA 289
 422 TGGCTTTGGACTGTCCATCGCTCAGCTCATCGATGTGATGAGAGAACCAATGATGA 481
 290 CCACCAACATTGGCTGCAATGCTTGGACAGATCATATTATACAGTGGAAATGTGTGAG 349
 482 CCACCAACGCTGGCTAAACAGAGAGTGGAGCGACTACAACTGGGCTGGAAACCCCGCTG 541
 350 AATATCCAGGGGTGAGACTGTTCTTTCCAGATGGCCAGATTTGGAAACCCAGCATTC 409
 542 ATTTTGGCAACATCATCTCTCAGGGTCCCTTCTGAGATCTGGATCCCGACATG 601
 410 TTCTCTATAACAGTGTGATGAGCGCTTTGAGCGCACATTCACACTAACGTTGTTGA 469
 602 TTCTCTACACAAANNITGGGAG---TTTGGAGTACCCACATGACCAAGGCCACCTCT 658
 470 ATTCTTTGGGCAATGGCCAGTACCTGCTCCAGGAGCATTTCAAGAGTTCCTGCTACATCG 529
 659 TCTCCAGCGGCACTGTGCACTGGGTGCCCCCGGCCATCTTACAGAGCTCTGCGAGATCG 718
 530 ATGTACGCTGGTTTCCCTTTGATGTGACACTGCAACTGAACTTGGTCTCTGCTCTT 589
 719 AGCTCACCTTCTTCCCTTCGACCGAGCAATGCAAGATGAAGTTTGGCTCTGAGACT 778
 590 ACGGAGGCTGGTCTTGGATCTGAGATGCAGAG-----GCAGATATCAGTGGCTATA 643

779 ATGACAAAGCCAAAGATCGACCTGGAGCAGATGAGCAGACTGTGACCTGAAGGACTACT 838
 644 TCCCAATGGAGATGGGACCTAGTGGGAATCCCGGCAAGAGAGTGAAGTTCTATG 703
 839 GGGAGAGCGGAGTGGGCAATCGTCAATGCCACGCGACCTACACAGCAAGAGTACG 898
 704 AGTGTCTGAAAGAGCCCTACCCGATGTCACTTCACTGACCTGACCTGCGCGCAGACGC 763
 899 ACTGTGCGCCGAGATCTTACCCGAGCTCACCTACGCTTGTCTATCCGCGGCTGCCGC 958
 764 TCTACTATGGCCTCAACCTGTGATCCCTGTGTGCTCATCTCCGCGCTTCCGCTCTGTG 823
 959 TCTTCTACACCATCAACCTCATATCCCTGCTGCTCATCTCTCTGCTCACTGTGCTGG 1018
 824 TGTCTCTGCTTCTGCAAGATTCGGGGAGAAATTTCCCTGGGATAAAGTCTTACTCT 883
 1019 TCTTCTACCTGCTCCGACTCGCGGAGAAATCACGTGTGCTATTTCCGCTGCTCTGT 1078
 884 CTCTTACCGCTTTCATGCTGCTGCTGAGATCATGCGCGCAACATCCGATTCGGTAC 943
 1079 CACTCACCGTCTTCTGCTGCTCATCTGAGATCATCTGCTCCACTCGTGTGCTCATCC 1138
 944 CATTTAGTACCCAGTACTTTCGCCAGCACCATGATCATCTGTGGCCTCTCTGCTGTG 1003
 1139 CGCTCATCGCGAGTACTGCTGTTCCATGATCTTCTGCTACCTGTCCATGCTCATCA 1198
 1004 CGGTGATGCTGTGAGTACCAACACGACGACCGCGGGGCAAGATGCCCAAGTGA 1063
 1199 CCGTCTTCTGCTCAATGTGGACCCGCTTCCCGAGACCCACACCATGCCCATCTGGG 1258
 1064 CCAGAGTCTATCTTCTGAACTGCTGCGGTGCTTCTTCTGAAATGAAGAGCCCGGGAGG 1123
 1259 TGGCGGGGCGCTTCTTGGGCTGTGTGCCCGGTGGCTTCTGATGAACCGGCGCCACAC 1318
 1124 ACAAGTGGCCCGGCTTCCACGACAAGCAGCGGCGCTGACGCTTGGCCAGTGTGGAGA 1183
 1319 CCGTGGAGCTCTGCCACCCCTTACGCTGAAAGCTCAGCCCTCTTATCACTGGCTGAGA 1378
 1184 TGAGCGCGTGGCGCGCGCGCCCGCCAGCAACCGGACCTGCTGTATCATCGGCTTCCGCG 1243
 1379 GCAACCTGATGATCGGAGGAGGAGTGTGTGGAGGAGGAGAGATGGGATGTG 1438
 1244 GCCTGGAGCGCTGCACTGTGTCCGACCCCGACTCTGGGTGATGTGTGGCGCATGG 1303
 1439 CAGGTGATGTGGCGCGCTCTGTGGGCACTCTCTGAGCCACGCGCACTGCACTGTGGGG 1498
 1304 CTTGCTCCCCACGACGATGAGCACTCTGTGACGCGGCGGCAACCCCGCGAGGGGAGCC 1363
 1499 CTTGAGTCCCAAGGCTGAGGCTCTGCTGAGGAGGAGTGTGCTGTCTATC-----AC 1552
 1364 CGGACTTGGCCAAAGATCTCGAGGAGTCCGCTACATTGCAATTCGCTTCCGCTGCCAGG 1423
 1553 CCCACATGCAAGAGCACTGGAAGTGTGCACTACATTTGCGGACCACTGGGCTCTGAGG 1612
 1424 ACAGAAAGCGGCGGCTTGCAGCGAGTGGAAATTCGCGCGCTGTGTGGTGGACCGCTGT 1483
 1613 ATGCTGACTCTTCGTTGAAGGAGGACTGGAATATGTTGCGCATGCTCATCGACAGGATCT 1672
 1484 GCCTCATGGCGCTTCTCGGTCTTACCATCATCTGCAACATCGGATCTCTGATGTC 1538
 1673 TCCTCTGCTGCTTTTATCATGCTGTCTTCTGCGGAGCAATCGGCTCTTCTGCTCC 1727

RESULT 14

US-08-700-636-1
 ; Sequence 1, Application US/08700636
 ; Patent No. 5910582
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,636
 ; FILING DATE: 16-JUL-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reiter, Stephen E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9368
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-546-4737
 ; TELEFAX: 619-546-9392
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2068 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 166..1752
 ; US-08-700-636-1

Query Match 18.4%; Score 345.8; DB 2; Length 2068;
 Best Local Similarity 54.1%; Pred. No. 1.6e-75;
 Matches 776; Conservative 0; Mismatches 644; Indels 15; Gaps 3;

QY	110	CGCGTCTGCTCTGACGCTGCTCCCTCAAGGCGAGTTCAGAGAGAGCTTTACAGAGAGC 169
DB	302	CCACGCGATTCGCGAGGAGGCTCGCATACCGAGACTGAGGACCGGCTTTCAACACC 361
QY	170	TGGTCAAGAACTACAAATCCCTTGGAGAGCGCCGTGGCCCAATGACTCGCAACCACTCACCG 229
DB	362	TCTTCCGGGGCTACAACCGCTGGGGCGCGCCGGTGCCCAACTTCAGACGTGGTGAATTG 421
QY	230	TCTACTTCTCCCTGAGCCTCCTGCAGATCATGACGTGATGAGAGAGACCAAGTTTAA 289
DB	422	TGGGCTTTGGAGTGTCCATGCTCAGCTCATGATGTGGATGAGAGAGACCAATGATGA 481
QY	290	CCACCAACATTTGGCTGCAAAATGCTTTGACAGACATCACTATTATACAGTGGAAATGTCTCAG 349
DB	482	CCACCAACGCTGTGGCTAAACAGAGAGTGGAGCGACTACAACTGCGCTGGAACCCCGCTG 541
QY	350	AATATCAGGGGTGAAGACTGTTGCTTTCCAGATGGCCAGATTTGGAAACCAAGACATTC 409
DB	542	ATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGAGATGATCTGATATCCCGACATTG 601
QY	410	TTCTCTATACAGTGTGATGAGCGCTTTTCAGCCACATTCACACATTAAGTGTGGTGA 469
DB	602	TTCTCTACAAACAAANTGGGGAG---TTTGAAGTACCCACATGACCAAGGCCCACTCT 658
QY	470	ATTCTTCTGGGCAATGGCAGTACCTGCTCCAGGCATATTTCAAGAGTTCTGCTACATCG 529
DB	659	TCCTCCAGGCACTGTGCACTGGGTGCCCCGGCCATCTACAGAGCTCTGTCAGCATCG 718
QY	530	ATGTACGCTGGTTTCCCTTTGATGTGAGCACTGCAAACTGCAAGTTTGGGTCTCTGTCCT 589

DB	719	ACGTCACTTCTTCCCTTCGACCAGCAGAACTGCAAGATGAAGTTTGGCTCTGGACTT 778
QY	590	ACGAGGCTGCTTGGATCTGCAGATGCAGGAG-----GCAGATATCAGTGGCTATA 643
DB	779	ATGACAGGCCAAGATCGACTTGGAGCAGATGGAGCAGACTGTGACCTGAAGGACTACT 838
QY	644	TCCCAATGGAGATGGGACCTTAGTGGAAATCCCGGCAAGAGGTGAAGGTTCTATG 703
DB	839	GGGAGAGCGGAGTGGGCCATCGTCAATGCACGGGCACCTACAAACAGCAAGAGTAGC 898
QY	704	AGTGTGCAAGAGCCCTTACCCGATGTCACCTTACAGATGACCATGCGCGCAGAGCGC 763
DB	899	ACTGTGCGGAGATCTACCCGACGTCACCTAGCCCTTGTCTATCCGGGGTCCGCGC 958
QY	764	TCTACTATGGCTCAAACTGTGTGATCCCTGTGTGCTCATCTCGGCCCTCGCCCTGTGG 823
DB	959	TCCTTACACCATCACTCATCTCCCTGCTCATCTCTCTGCTCATCTCTGCTGTGG 1018
QY	824	TGTTCTGCTTCTGCGAGATTCGGGGGAGAGATTTCCCTGGGGATACAGTCTTACTCT 883
DB	1019	TCCTTCTACCTGCCCTCCGACTCGCGGAGAGATCACTGTGCAATTTGGGTGCTGTGT 1078
QY	884	CTCTTACCGTCTTCTCATGCTGCTCGTGGCTGAGATCATCCCGCAACATCCGATTCGGTAC 943
DB	1079	CACCTACCGTCTTCTGCTGCTCATCTGAGATCATCCCGTCCACCTGCTGCTGCTATCC 1138
QY	944	CATTGATAGCCGAGTACTTCGCCAGCACCATGATCATCTCGTGGGCTCTCGGTGGTGA 1003
DB	1139	CGCTCATCGGCGAGTACCTGTGTTTCCATCATCTTCTGTCACCTGCTGCTCATCA 1198
QY	1004	CGGTGATCGTGTGAGTACACACACAGACCCCGAGCGGGGCAAGATGCCAAGTGA 1063
DB	1199	CGGTCTGCTGCTCAATGTGGACCACTCCCGCAGCACCCACACCATGCCCCACTGG 1258
QY	1064	CCAGAGTCACTCTTCTGAATCTGCTCGGTGCTTCTCTCGAATGAAGAGCGCCGGGAGG 1123
DB	1259	TGCGGGGGGCTTCTTGGGCTGTGTGCCCCCGTGTCTGATGAACCGGCCCGCCACAC 1318
QY	1124	ACAAGGTGCGCCGCGCTGCCAGCAACAGCAGCGGCTGTGAGCTGCGGCTGAGTGTGTGGCCGCTATG 1378
DB	1319	CGTGGAGCTCTGCCACCCCTTACGCTGAGCTCAGCCCTTCTTATCACTGGCTGGAGA 1378
QY	1184	TGAGCGCGTGGCGCGCGCCCGCCAGCAACCGGAACTGCTGTACATCGGCTTCCGCG 1243
DB	1379	GCAACGTGATCCGAGGAGAGAGGAGTGTGTGGAGAGGAGGACAGATGGGCAATGTG 1438
QY	1244	GCCTGGAGCGCTGCACTGTGCTCCGACCCCGACTCTCGGGGTAGTGTGTGGCCGCTATG 1303
DB	1439	CAGGTCACTGGCCCGCTCTGTGGGCACTCTGTGACGACCGCCACCTGCACTCTGGGG 1498
QY	1304	CCTGCTCCCGCCAGCAGATGAGCACCTCTCTGACGCGGGGCAACCCCGGAGGGGAGCC 1363
DB	1499	CCTCAGGTCCCAAGGCTGAGGCTCTGCTGACGAGGCTGAGCTGTGCTATC-----AC 1552
QY	1364	CGGACTTGGCCAGATCTCTGGAGGAGTCCGTACTATTGCGCAATCGTTCCGCTGCCAG 1423
DB	1553	CCACATGCAAGAGGCACTGGAAGGTGCACTACATTCCCAACACCTTGGGCTGTGAGG 1612
QY	1424	ACGAAAGCAGGCGGTCTGACGAGTGAAGTTCGCGCCCTGTGTGGTGGAGCCGCTGT 1483
DB	1613	ATGTGCACTTCTGGTGAAGAGGACTGGAAGTATGTTGCCATGGTTCATCGACAGATCT 1672
QY	1484	GCCTCATGCGCTTCTCGGTCTTCAACCATCATGCAACCATCGGCATCTGATGATGC 1538
DB	1673	TCCTCTGGCTGTTTATCATCTGCTTCTTCTGGGACCATCGGCTCTTCTTCTGCC 1727

RESULT 15
 US-08-467-574-1
 ; Sequence 1, Application US/08467574
 ; Patent No. 6022704
 ; GENERAL INFORMATION:
 ; APPLICANT: Eliot, Kathryn J.

APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 166..1752
US-08-467-574-1
Query Match 18.4%; Score 345.8; DB 3; Length 2068;
Best Local Similarity 54.1%; Pred. No. 1.6e-75;
Matches 776; Conservative 0; Mismatches 644; Indels 15; Gaps 3;
Qy 110 CCGGTGCTCCTGACGTGCTCCCTGGAAGGAGTTCAGAGGAGCTTTACAGGAGC 169
Db 302 CCACGGCAATGCGCAGGAGGCTCGCATACGAGACTGAGACCGGCTCTTCAACACC 361
Qy 170 TGGTCAAGAACTACAACTCCCTGGAGAGCCCGTGGCCAAATGACTCGCAACCACTCACCG 229
Db 362 TCTTCGGGGCTACAAACGCTGGGCGCGCGGTGCCCAACACTTCAGACGTGGTGATTG 421
Qy 230 TCTACTTCTCCCTGAGCCTCTCTGAGATCATGCACTGATGAGAGTGAAGAACCAAGTTTAA 289
Db 422 TGCCTTTGGACTGCTCCATCGCTCAGCTCATGATGTGGATGAGAGAAACCAATGATGA 481
Qy 290 CCACCAACATTTGGCTGCAATGTCTTGACAGATCACTATTACAGTGGATGTGTAG 349
Db 482 CCACCAACCTCTGGCTTAAACAGGAGTGGAGCACTTACAACTGGGCTGGAAACCCCGCTG 541
Qy 350 AATATCCAGGGGTGAAGACTGTTCGTTTCCAGATGGCCAGATTTGGAACCAAGACATTC 409
Db 542 ATTTTGGCAACATCACTCTCAGGGTCCCTCTTGAGATGATCTGGATCCCGCATTTG 501
Qy 410 TTCTCTATAACAGTGTGATGAGCGCTTTGACGCCACATTCACACTAAGCTGTGGTGA 469
Db 602 TTCTCTACAAACAAANNITGGGAG---TTTGCAGTGACCCACATGACCAAGGCCACCTCT 658
Qy 470 ATTCTTCTGGGCATTCGCCAGTACCTGCTCCAGGCATATTCAAGATTCTCTGCTACATCG 529

Db 659 TCTCCACGGGCACTGTGCACTGGTGCCTCCCGGCCATCTTACAGAGCTCCTCAGCATCG 718
Qy 530 ATGTACGCTGTTTCCCTTTTGTATGTCAGCACTGCAAACTGAAGTTTGGTCTCTGCTCT 589
Db 719 AGTCACTTCTTCCCTTCGACGAGCAACTGCAAGATGAAGTTTGGCTCTGACAT 778
Qy 590 ACGGAGGCTGCTCTTGGATCTGCAAGATGACAGAG-----GCAGATATCAGTGGCTATA 643
Db 779 ATGACAAAGCCAAAGATCGACCTGGAGCAGATGGAGCAGACTGTGACCTGAAGGACTACT 838
Qy 644 TCCCCAATGAGATGGGACCTAGTGGGAATCCCGGCAAGAGGAGTGAAGTTCTATG 703
Db 839 GGGAGAGCGGCGAGTGGGCCATCGTCAATGCCACGGGCACTTACAAACAGAAAGTACG 898
Qy 704 AGTCTGCAAAAGAGCCCTTACCCCGATGTCACTTTCACAGTGACCATGCGCCGAGAACGC 763
Db 899 ACTGCTGCGCGAGATCTACCCGACGTCACTACGCTTCGTTCATCGCGGCTGCGCG 958
Qy 764 TCTACTATGGCCTCAACCTGCTGATCCCTGTGTGTCTCATCTCGGCCCTGCGCTGCTGG 823
Db 959 TCTTCTACACCAATCAACCTCATCATCCCTGCTGCTCATCTCTGCTCACTGTGCTGG 1018
Qy 824 TGTTCCTGCTTCTGTCAGATTCGGGAGAGATTTCCCTGGGGATAACAGTCTTACTCT 883
Db 1019 TCTTCTACCTGCTCCGACTGCGGCGAGAGATCAGCTGTGCATTTGCTGCTGCTGT 1078
Qy 884 CTCTTACCGTCTTTCATGCTGCTGCTGAGATCATGCCCCGCAACATTCGATTCGGTAC 943
Db 1079 CACTCACCGTCTTCTGCTGCTCATCACTGAGATCATCCGTCACCTCGTGTGCTCATCC 1138
Qy 944 CATGTAGCCAGTACTTCGCGAGACCATGATCATCTGGGCTCTCGTGGCTGTGTA 1003
Db 1139 CGCTCATCGCGGAGTACTGCTGTTTCAACCATGATCTTCGTACCCCTGCTCATCTGTA 1198
Qy 1004 CGGTGATCGTGTGCTGATACACCAACCGACCGGCGGCAAGATGCCCAAGTGA 1063
Db 1199 CCGTCTTCTGCTCAATGTGGAACACGCTCCCCAGCACCCACCATGCCACTGGG 1258
Qy 1064 CCAGAGTCACTCTTGTGAATGTGTGCGGTGCTTCTSCGAATGAAGAGCCCGGGAGG 1123
Db 1259 TCGGGGGGCGCTTCTGGGCTGTGTGCGCGGTGCTTCTGATGAACCGGCGCCACCAC 1318
Qy 1124 ACAAGTGTGCGCGGCTGTCAGCAACAGCAGCGGCTGCGAGCTGCGAGTGTGAGA 1183
Db 1319 CCGTGGAGTCTTGCCACCCCTTACGCTGAAGTCTCAGCCCTCTTATCATCTGGCTGAGA 1378
Qy 1184 TGAGCGCGTGGCGCGCCCGCCAGCAACCGGGAACCTGCTGTATCATCGGCTTCCGCG 1243
Db 1379 GCACTGTGATGCCGAGAGGAGGAGGTGTGTGGAGAGGAGGAGAGATGGGCACTGTG 1438
Qy 1244 GCCTGGAAGCGGTGCACTGTGTCCGACCCCGACTCTGGGGTGTGTGTGGCGCATGG 1303
Db 1439 CAGGTCACTGTGGCGCCCTCTGTGGGCACTCTGACGCAACCGGCACTGTGCACTGTGGG 1498
Qy 1304 CTTGCTCCCGCACGATGAGCACCTCTGTCAGCGCGGCAACCCCGGAGGGGAGCC 1363
Db 1499 CCTCAGGTCCCAAGCTGAGCTCTGCTGAGAGGAGTGTGCTGTGCTATC-----AC 1552
Qy 1364 CGGACTTTGGCCAAAGATCCTGGAGAGGTCCGCTACATTTGCCAATTCGCTTCGCTGCGCAGG 1423
Db 1553 CCCACATGCAAGGCACTGGAAGTGTGCACTACATATTCGCGCACTCTGCGGTCTGAGG 1612
Qy 1424 ACGAAAGGAGCGGTCTGACGCGAGTGAAGTTCGCGGCTGTGTGGTGTGAGACCGCTGT 1483
Db 1613 ATGCTGACTCTTCGTTGAAGGAGGACTGGAAGTATGTTGCCATGCTTCATCCAGAGATCT 1672
Qy 1484 GCCTCATGGCTCTTCGCTTTCACCATCATCTGCACCATCGGATCTCTGATGTC 1538
Db 1673 TCCTCTGCTGTTTATCATCTGCTTCTCTGGGACCAATCGGCTCTTCTTCTGCC 1727

Search completed: May 8, 2004, 22:05:28

Job time : 160 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 15:49:02 ; Search time 781 Seconds
(without alignments)
10204.378 Million cell updates/sec

Title: US-09-703-951a-11

Perfect score: 1876

Sequence: 1 GCGCGCAGCGCAGCGCGG.....TGCCTGGAAGCCCTTCGGA 1876

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1875.6	100.0	1876	2	AAV12197 Human neu
2	1875.6	100.0	1876	2	AAT48239 Neuronal
3	1875.6	100.0	1876	6	AB54875 Human neu
4	1875.6	100.0	1876	6	ABV73248 Human neu
5	1875.6	100.0	1876	8	ADA10864 Human neu
6	1787	95.3	1964	6	ABZ11298 Human pol
7	1543	82.2	1590	4	AAV44687 V274T var
8	1508.6	80.4	1509	4	AAC90380 Wild-type
9	1507	80.3	1509	4	AAC90385 Mutant hu
10	1507	80.3	1509	4	AAC90386 Mutant hu
11	1505.4	80.2	1509	3	AAC58395 Human PRO
12	1505.4	80.2	1509	4	AAC90387 Mutant hu
13	1279	68.2	2511	5	AAS79730 DNA encod
14	958.4	51.1	2769	4	AAT59196 Neuronal
15	743.2	39.6	1416	4	AAC90382 Chimeric
16	647	34.5	2101	2	AAT59197 Neuronal
17	512.2	27.3	368	4	AAB34275 Human col
18	405.2	21.6	3700	3	AAZ24476 H. viresc
19	376	20.0	3109	3	AAT24477 Human neu
20	362.2	19.3	2277	2	AAV12199 Human neu
21	362.2	19.3	2277	2	AAQ90387 Alpha 2 s
22	362.2	19.3	2277	6	AB54870 Human neu
23	362.2	19.3	2277	6	ABV73243 Human neu

24	362.2	19.3	2664	2	AAT48235	Neuronal
25	362.2	19.3	2664	6	ABK92165	Prostate
26	362.2	19.3	2664	8	ADA10854	Human neu
27	362.2	19.3	2664	9	ADC71170	Human 205
28	362.2	19.3	2666	9	ADC71168	Human 205
29	333.4	17.8	337	2	AAK56154	Human alp
30	306.4	16.3	2082	2	AAT59527	Alpha4 su
31	305.6	16.3	936	4	ABL13733	Drosophil
32	304.8	16.2	2082	2	AAT59528	Alpha4 su
33	304.8	16.2	2752	9	ADB78671	Human nic
34	304.8	16.2	2752	9	ADB78670	Human nic
35	304.8	16.2	2752	9	ADB78661	Human nic
36	304.8	16.2	2752	9	ADB78672	Human nic
37	304.8	16.2	2752	9	ADB78663	Human nic
38	304.8	16.2	2752	9	ADB78669	Human nic
39	304.8	16.2	2752	9	ADB78662	Human nic
40	304.8	16.2	2752	9	ADB78673	Human nic
41	304.8	16.2	3343	9	ADE85024	Farnesyl
42	304.8	16.2	3496	2	AAT48237	Neuronal
43	304.8	16.2	3496	8	ADA10858	Human neu
44	303.2	16.2	1809	5	AAS91552	DNA encod
45	303.2	16.2	2752	9	ADB78660	Human nic

ALIGNMENTS

RESULT 1

AAV12197

ID AAV12197 standard; cDNA; 1876 BP.

XX AC AAV12197;

XX DT 14-MAY-1998 (first entry)

XX DE Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.

XX Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
KW brain tissue; screening; NACR; antibody; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 73..1581
FT /*tag= a
FT /product= "neuronal nicotinic acetylcholine receptor
FT alpha-7 subunit"

XX PN WO9420617-A2.

XX PD 15-SEP-1994.

XX PF 08-MAR-1994; 94WO-US002447.

XX PR 08-MAR-1993; 93US-00028031.

XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

XX PI Elliott KJ, Ellis SB, Harpold WM;

XX DR WPI; 1994-303024/37.

XX DR P-PSDB; AAW44153.

XX Human neuronal nicotinic acetylcholine receptor subunits and DNA - also
XX transformed cells useful for screening cpds. which modulate activity of
XX the receptor.
XX Claim 8; Page 78-79; 99pp; English.
XX The present sequence encodes a human neuronal nicotinic acetylcholine
XX receptor (NACR) subunit. The cells expressing the alpha and/or beta
XX NACR subunits may be used in a method of screening compounds to identify
XX any which modulate the activity of human neuronal NACR. Subunit specific

AAT48239
 ID AAT48239 standard; DNA; 1876 BP.
 XX AC AAT48239;
 XX DT 09-APR-1997 (first entry)
 XX DE Neuronal nicotinic acetylcholine receptor alpha-7 subunit DNA.
 XX KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 XX FT 73..1581
 XX FT /*tag= a
 XX PN WO9641876-A1.
 XX PD 27-DEC-1996.
 XX PF 07-JUN-1996; 96WO-US009775.
 XX PR 07-JUN-1995; 95US-00484722.
 XX PA (SIBI-) SIBIA NEUROSCIENCES INC.
 XX PI Elliott KJ, Harpold MM;
 XX DR WPI; 1997-065463/06.
 XX DR P-PSDB; AAM09025.
 XX PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units - used
 XX PT in screening to determine the effect of drugs on the receptor.
 XX PS Disclosure; Page 71-73; 108pp; English.
 XX CC A DNA sequence (AAT48239) codes for the alpha-7 subunit (AAM09025) of the
 CC human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp.
 CC mammalian cells or amphibian oocytes, carrying alpha-7 nucleic acids,
 CC opt. in combination with other alpha and/or beta subunit nucleic acids
 CC (see also AAT48232-38, AAT48240-41), express recombinant nAChR subunits
 CC useful for identifying cpds. that modulate the activity of human nAChRs
 XX SQ Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1875.6; DB 2; Length 1876;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1875; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGC CGCAGGCGGAGGCGCGGCGACAGCGGAGCGGCGCGGCTCGCTGCGAGCT 60
 DB 1 GGC CGCAGGCGGAGGCGCGGCGACAGCGGAGCGGCGCGGCTCGCTGCGAGCT 60
 QY 61 CCGGGACTCAACATGCGCTCTCGCGGAGGCGCTCGCTGCGGCGCGGCTCGCTC 120
 DB 61 CCGGGACTCAACATGCGCTCTCGCGGAGGCGCTCGCTGCGGCGCGGCTCGCTC 120
 QY 121 CTGCACTGTCCTGCAAGCGGAGTTCCAGAGAGCTTTACAGAGCTGTTCAAGAAC 180
 DB 121 CTGCACTGTCCTGCAAGCGGAGTTCCAGAGAGCTTTACAGAGCTGTTCAAGAAC 180
 QY 181 TACAATCCCTTGGAGAGGCGCGTGGCAATGACTCGCAACCTACCGCTCTACTTCTCC 240
 DB 181 TACAATCCCTTGGAGAGGCGCGTGGCAATGACTCGCAACCTACCGCTCTACTTCTCC 240
 QY 241 CTGAGCCTCTGCGAGATCATGGAGCTGGATGAGAGAACCAAGTTTTAACCAACCAATT 300
 DB 241 CTGAGCCTCTGCGAGATCATGGAGCTGGATGAGAGAACCAAGTTTTAACCAACCAATT 300
 QY 301 TGGCTGCAATGCTTGGACAGATCACTATTATACAGTGGATGTTGTCAGATATCCAGGG 360

Db TGGCTGCAATGCTTGGACAGATCACTATTATACAGTGGATGTTGTCAGATATCCAGGG 360
 QY GTGAAGACTGTTGTTTCCAGATGGCCAGATTGGAAACAGACATCTTCTCTATAAC 420
 Db GTGAAGACTGTTGTTTCCAGATGGCCAGATTGGAAACAGACATCTTCTCTATAAC 420
 QY AGTCTGATGAGCGCTTTGACGCCACATTCACACTAACCGTGTGGTGAATCTTCTGGG 480
 Db AGTCTGATGAGCGCTTTGACGCCACATTCACACTAACCGTGTGGTGAATCTTCTGGG 480
 QY CATTCGCACTGCTGCTCCAGGCAATTCAGAGTTCCTGCTACATCATGATGATGCTGG 540
 Db CATTCGCACTGCTGCTCCAGGCAATTCAGAGTTCCTGCTACATCATGATGATGCTGG 540
 QY TTTCCCTTTGATGTGACGACTGCAAACTGAAGTTTGGGTCTCTGCTTACGAGGCTGG 600
 Db TTTCCCTTTGATGTGACGACTGCAAACTGAAGTTTGGGTCTCTGCTTACGAGGCTGG 600
 QY TCCTTGGATCTGCAGATGCAGAGGAGATATCAGTGGCTATATCCCAATGGAGATGG 660
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 QY GACCTAGTGGGAATCCCGGCAAGAGGAGTGAAGGTTCTATGAGTGTCTGCAAGAGGCC 720
 Db GACCTAGTGGGAATCCCGGCAAGAGGAGTGAAGGTTCTATGAGTGTCTGCAAGAGGCC 720
 QY TACCCCGGATGCACCTTCACAGTACCATGCGCGCAGGAGCTCTACTATGCGCTCAAC 780
 Db TACCCCGGATGCACCTTCACAGTACCATGCGCGCAGGAGCTCTACTATGCGCTCAAC 780
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 Db CTGCTGATCCCTGTGTGCTCATCTCCGCTCGCCCTGCTGGTGTCTGCTGCTGCA 840
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 QY CTGCTCTGCTGCTGATCATGCCCCGCAACATCCGATTCGGTACCATTTGATAGCCAGTAC 960
 Db CTGCTCTGCTGCTGATCATGCCCCGCAACATCCGATTCGGTACCATTTGATAGCCAGTAC 960
 QY TTCGCGCAGCACCATGATCATCTCGTGGGCTCTCGTGGTGGTGCACCGTGTGCTGCGAG 1020
 Db TTCGCGCAGCACCATGATCATCTCGTGGGCTCTCGTGGTGGTGCACCGTGTGCTGCGAG 1020
 QY TACCAACACACGACCCCGAGCGGGGCAAGATGCCCAAGTGACACAGAGTCTCTCTCTG 1080
 Db TACCAACACACGACCCCGAGCGGGGCAAGATGCCCAAGTGACACAGAGTCTCTCTCTG 1080
 QY AACTGTGCGCGTGGTTCCTSCGAATGAAGAGGCGCGGGAGGACAAGGTGCGCCCGGCC 1140
 Db AACTGTGCGCGTGGTTCCTSCGAATGAAGAGGCGCGGGAGGACAAGGTGCGCCCGGCC 1140
 QY TGGCAGCAACAGAGGCGGCTGCGAGCTGCGCAGTGTGAGATGAGCGCGTGGCGCGG 1200
 Db TGGCAGCAACAGAGGCGGCTGCGAGCTGCGCAGTGTGAGATGAGCGCGTGGCGCGG 1200
 QY CCGCGCGCAGCAAAACCGGAACTCTGTGTATCATCTCGGCTTCGCGGCTGAGACGCGTGCAC 1260
 Db CCGCGCGCAGCAAAACCGGAACTCTGTGTATCATCTCGGCTTCGCGGCTGAGACGCGTGCAC 1260
 QY TGTGTCCCAACCCCGACTCTGCGGCTGAGTGTGCGCGCATGCGCTGCTGCTGCTGCTG 1320
 Db TGTGTCCCAACCCCGACTCTGCGGCTGAGTGTGCGCGCATGCGCTGCTGCTGCTGCTG 1320
 QY GATGAGCACTCTGCAACGCGGGCAACCCCGGAGGGGAGCCCGGACTTGGCCAAAGATC 1380
 Db GATGAGCACTCTGCAACGCGGGCAACCCCGGAGGGGAGCCCGGACTTGGCCAAAGATC 1380
 QY CTGAGGAGGCTCGCTTACATTTGCAATCGCTTCCGCTGCGCAGGACGAAACGAGGCGGTC 1440
 Db CTGAGGAGGCTCGCTTACATTTGCAATCGCTTCCGCTGCGCAGGACGAAACGAGGCGGTC 1440

FT	3'UTR	1585..1876 /*tag= c
FT	XX	US6524789-B1.
PX	XX	25-FEB-2003.
PD	XX	07-JUN-1996; 96US-00660451.
PF	XX	07-JUN-1995; 95US-00484722.
XX	XX	(MERI) MERCK & CO INC.
XX	PI	Elliott KJ, Harpold MW;
PI	XX	WPI; 2003-511917/48.
DR	XX	P-PSDB; ADA10874.
XX	XX	New nucleic acid encoding an alpha-6 or a beta-3 subunit of a human neuronal nicotinic acetylcholine receptor (nAChR), useful for identifying compounds that modulate human neuronal nAChR activity.
PT	XX	Claim 33; Col 67-72; 63pp; English.
PS	XX	The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding an alpha 6 or a beta 3 subunit of a human neuronal nicotinic acetylcholine receptor nAChR. nAChR's form ligand-gated ion channels that mediate synaptic transmissions between nerve and muscle and between neurons upon interaction with the neurotransmitter acetylcholine. The nucleic acid molecule is useful for identifying compounds that modulate human neuronal nAChR. The present sequence represents DNA encoding the human neuronal nicotinic acetylcholine receptor, nAChR, alpha 7 subunit. Note: the present sequence decodes to the protein shown in ADA10874 not the one described in the specification as being the nAChR alpha 7 subunit ADA10865.
CC	XX	Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 U; 0 Other;
SQ	XX	Query Match 100.0%; Score 1875.6; DB 8; Length 1876; Best Local Similarity 99.9%; Pred. No. 0; Matches 1875; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1	GCGGAGGGGAGGCGCGGGGAGACGCGAGAGCTGGAGCGGCCGGCTGCCTCAGCT 60
Db	1	GCGGAGGGGAGGCGCGGGGAGACGCGAGAGCTGGAGCGGCCGGCTGCCTCAGCT 60
Qy	61	CAGGACTCAACATGCCTGCTCCCGGAGGGCGCTGGCTGGCGCTGGCGCGCTCGCTC 120
Db	61	CAGGACTCAACATGCCTGCTCCCGGAGGGCGCTGGCTGGCGCTGGCGCGCTCGCTC 120
Qy	121	CTGCACGTGTCCTGCAGGCGAGTTCCAGGGAAGCTTTCACAGGAGCTGGTCAAGAAC 180
Db	121	CTGCACGTGTCCTGCAGGCGAGTTCCAGGGAAGCTTTCACAGGAGCTGGTCAAGAAC 180
Qy	181	TACAATCCCTTGAGAGCGCCGCTGCGCAATGACTCGCAACCACCTCACCTCTCTCC 240
Db	181	TACAATCCCTTGAGAGCGCCGCTGCGCAATGACTCGCAACCACCTCACCTCTCTCC 240
Qy	241	CTGAGCTCTCTGCAGATCATGGACGTGGATGAGAAGAACCAAGTTTTAAACCAAAATT 300
Db	241	CTGAGCTCTCTGCAGATCATGGACGTGGATGAGAAGAACCAAGTTTTAAACCAAAATT 300
Qy	301	TGGCTGGAATGCTTGGACAGATCACTATTACAGTGGATGTCAGATATCCAGGG 360
Db	301	TGGCTGGAATGCTTGGACAGATCACTATTACAGTGGATGTCAGATATCCAGGG 360
Qy	361	GTGAAGACTGTTCTGTTTCCCAGATGCGCCAGATTTTGGAAAACAGACATTTCTCTATAAC 420
Db	361	GTGAAGACTGTTCTGTTTCCCAGATGCGCCAGATTTTGGAAAACAGACATTTCTCTATAAC 420
Qy	421	AGTGTGTATGAGCGCTTTGACGCCACATTCACACTAAAGTGTGGTAATCTTCTGGG 480
Db	421	AGTGTGTATGAGCGCTTTGACGCCACATTCACACTAAAGTGTGGTAATCTTCTGGG 480

Db	779	CGGGGAGAGATTCCCTGGGGATAACAGTCTTCTCTTACCGTCTTCACTGCTGT 838
Qy	906	CGTGGCTGAGATCATGCCGCCCAACATCCGATTCGGTACCAATTGATACCCAGTACTTCGC 965
Db	839	CGTGGCTGAGATCATGCCGCCCAACATCCGATTCGGTACCAATTGATACCCAGTACTTCGC 898
Qy	966	CAGACCAATCATCATCGTGGGCCCTCTCGGTGGTGGTGAACGGTCAATCGTGTGCAGTACCA 1025
Db	899	CAGACCAATCATCATCGTGGGCCCTCTCGGTGGTGGTGAACGGTCAATCGTGTGCAGTACCA 958
Qy	1026	CCACACGACCCCGACACGGGGGCAAGATGCCCCAAGTGCACAGAGTCAATCTTCTGAACATG 1085
Db	959	CCACACGACCCCGACACGGGGGCAAGATGCCCCAAGTGCACAGAGTCAATCTTCTGAACATG 1018
Qy	1086	GTGGCGCTGTCTCTSCAATGAAGAGCCCGGGGAGGAACAAGTGGCCCGCGCTTGCCTCA 1145
Db	1019	GTGGCGCTGTCTCTSCAATGAAGAGCCCGGGGAGGAACAAGTGGCCCGCGCTTGCCTCA 1078
Qy	1146	GCAACAGCAGCGGGGCTCGACGCTGGCCAGTGTGGAGATCAGAGCCCGTGGCGCGCGCGCC 1205
Db	1079	GCAACAGCAGCGGGGCTCGACGCTGGCCAGTGTGGAGATCAGAGCCCGTGGCGCGCGCC 1138
Qy	1206	GCCAGCAACGGGAACCTGCTGTATCATCGGCTTCCGGCGCTGGAACGGCGTGCACATGTGT 1265
Db	1139	CGCCAGCAACGGGAACCTGCTGTATCATCGGCTTCCGGCGCTGGAACGGCGTGCACATGTGT 1198
Qy	1266	CCCGACCCCGACTCTCGGGTAGTGTCTGGCCGATCGCTGCTCCGCCACGACACATGA 1325
Db	1199	CCCGACCCCGACTCTCGGGTAGTGTGTGACCGCATGGCTTCTCCGCCACGACACATGA 1258
Qy	1326	GCACTCTCTGCAACGGCGGGCAACCCCGAGGGGGAACCGGACATGCGCCAAAGATCTCTGGA 1385
Db	1259	GCACTCTCTGCAACGGCGGGCAACCCCGAGGGGGAACCGGACATGCGCCAAAGATCTCTGGA 1318
Qy	1386	GGAGTCCGGCTACATTCGCAATCGCTTCCGCTGCCAGAGCAAGACGAGCGGTCTGCAG 1445
Db	1319	GGAGTCCGGCTACATTCGCAACCGCTTCCGCTGCCAGAGCAAGACGAGCGGTCTGCAG 1378
Qy	1446	CGAGTGAAGTTCCGCGCTGTGTGTGTGACCGCTGTGCTCATGAGCCCTTCTCGGTCTT 1505
Db	1379	CGAGTGAAGTTCCGCGCTGTGTGTGTGACCGCTGTGCTCATGAGCCCTTCTCGGTCTT 1438
Qy	1506	CACCATCATCTGCACCATCGGCATCTCGATGTGGCTCCCAACTCTGTGGAGCGCGTGC 1565
Db	1439	CACCATCATCTGCACCATCGGCATCTCGATGTGGCTCCCAACTCTGTGGAGCGCGTGC 1498
Qy	1566	CAAAAGACTTTGCGTAAACACACCGCTGGTTCTGTACATGTGGAAAACCTCACAGATGGGCAAG 1625
Db	1499	CAAAAGACTTTGCGTAAACACACCGCTGGTTCTGTACATGTGGAAAACCTCACAGATGGGCAAG 1558
Qy	1626	GCTTTGGCTTGGCGAGATTTGGGGGTGCTAATCCAGACAGCATTAACGCCACAATC 1685
Db	1559	GCTTTGGCTTGGCGAGATTTGGGGGTGCTAATCCAGACAGCATTAACGCCACAATC 1618
Qy	1686	CAGTGTTCCTTCTGGCTGTCAAGTCGTGTCTTACGGTTTCTTTGTTACTTTAGGTAGT 1745
Db	1619	CAGTGTTCCTTCTGGCTGTCAAGTCGTGTCTTACGGTTTCTTTGTTACTTTAGGTAGT 1678
Qy	1746	AGAACTCAGCACTTTGTTTCATATCTCAGATGGGCTGATAGATATCTCTTGGCAATCC 1805
Db	1679	AGAACTCAGCACTTTGTTTCATATCTCAGATGGGCTGATAGATATCTCTTGGCAATCC 1738
Qy	1806	GTACCATCGGTACGACGGGCCACTGAGTAGTCAATTTTGCCCAATAGGCCACTGCTCGAA 1865
Db	1739	GTACCATCGGTACGACGGGCCACTGAGTAGTCAATTTTGCCCAATAGGCCACTGCTCGAA 1798
Qy	1866	AGCCCTTCGGA 1876
Db	1799	AGCCCTTCGGA 1809

RESULT 7

Query Match 80.4%; Score 1508.6; DB 4; Length 1509;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1508; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	73	ATGCGCTCTCGCCGGAGGCGTCTGGCTGGCGCTGGCGGCTGCTCTCTGCACTGTC	132
Db	1	ATGCGCTCTCGCCGGAGGCGTCTGGCTGGCGCTGGCGGCTGCTCTCTGCACTGTC	60
QY	133	CTGCAAGCGAGTTCAGAGGAAGCTTTACAGGAGCTGGTCAAGAACTTACAATCCCTTG	192
Db	61	CTGCAAGCGAGTTCAGAGGAAGCTTTACAGGAGCTGGTCAAGAACTTACAATCCCTTG	120
QY	193	GAGAGCCGCTGCAATGACTCGCAACACTCAACGCTACTTCTCCCTGAGCCTCCTG	252
Db	121	GAGAGCCGCTGCAATGACTCGCAACACTCAACGCTACTTCTCCCTGAGCCTCCTG	180
QY	253	CAGATCATGCGAGTGGATGAGAACCAAGTTTAAACCAACAACTTGGCTGCAATG	312
Db	181	CAGATCATGCGAGTGGATGAGAACCAAGTTTAAACCAACAACTTGGCTGCAATG	240
QY	313	TCTTGGACAGATCACTATTATACAGTGGATGTGTCAGATATCCAGGGGTGAAGACTGT	372
Db	241	TCTTGGACAGATCACTATTATACAGTGGATGTGTCAGATATCCAGGGGTGAAGACTGT	300
QY	373	CGTTTCCAGATGGCCAGATTGGAAACAGACATCTTCTATPACAGTGTCTGATGAG	432
Db	301	CGTTTCCAGATGGCCAGATTGGAAACAGACATCTTCTATPACAGTGTCTGATGAG	360
QY	433	CGCTTTGAGCCACATTCACACTAAGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	492
Db	361	CGCTTTGAGCCACATTCACACTAAGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	420
QY	493	CTGCTCCAGGCATATTCAGAGTTCTCTGCTACATCGATGTACGCTGTTCCTTTGAT	552
Db	421	CTGCTCCAGGCATATTCAGAGTTCTCTGCTACATCGATGTACGCTGTTCCTTTGAT	480
QY	553	GTGAGCACTGCAAACTGAGTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	612
Db	481	GTGAGCACTGCAAACTGAGTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540
QY	613	CAGATGAGGAGGAGATATGAGTGGCTATATCCCAATGGAGATGGAGTGGAGTGGGA	672
Db	541	CAGATGAGGAGGAGATATGAGTGGCTATATCCCAATGGAGATGGAGTGGAGTGGGA	600
QY	673	ATCCCCGCAAGAGAGTGAAGTTCTATGAGTGTCTGCAAGAGCCCTTACCCCGATGTC	732
Db	601	ATCCCCGCAAGAGAGTGAAGTTCTATGAGTGTCTGCAAGAGCCCTTACCCCGATGTC	660
QY	733	ACCTTTCAGATGACCATGCGCGCAGAGAGCTTACTATGAGCTCAACCTGCTGATCCGC	792
Db	661	ACCTTTCAGATGACCATGCGCGCAGAGAGCTTACTATGAGCTCAACCTGCTGATCCGC	720
QY	793	TGTGTGCTCATCTCGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	852
Db	721	TGTGTGCTCATCTCGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780
QY	853	AAGATTTCCCTGGGATACAGTCTTACTCTCTTACCGTCTTCTATGCTGCTGCTGCTG	912
Db	781	AAGATTTCCCTGGGATACAGTCTTACTCTCTTACCGTCTTCTATGCTGCTGCTGCTG	840
QY	913	GAGATCATGCGCAACATCCGATTCGGTATGATGATGATGATGATGATGATGATGATGATG	972
Db	841	GAGATCATGCGCGCAACATCCGATTCGGTATGATGATGATGATGATGATGATGATGATG	900
QY	973	ATGATCATGCTGGCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1032
Db	901	ATGATCATGCTGGCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
QY	1033	GACCCCGAGCGGGCAAGATGCCAAGTGGACAGAGTCACTCTTCTGAACTGGTGGCGG	1092
Db	961	GACCCCGAGCGGGCAAGATGCCAAGTGGACAGAGTCACTCTTCTGAACTGGTGGCGG	1020

QY	1093	TGGTTCCTSCAATGAAG	1152
Db	1021	TGGTTCCTSCAATGAAG	1080
QY	1153	CAGCGGCGCTCAGCGCTGCGCAGTGTGAGATGAGCGCGCTGCGCGCGCGCGCGCGCAGC	1212
Db	1081	CAGCGGCGCTCAGCGCTGCGCAGTGTGAGATGAGCGCGCTGCGCGCGCGCGCGCGCAGC	1140
QY	1213	AACGGGAACCTGCTGTATCATCGGCTTCGCGCGCTTCGAGCGGCTGCACTGTGTCCCGACC	1272
Db	1141	AACGGGAACCTGCTGTATCATCGGCTTCGCGCGCTTCGAGCGGCTGCACTGTGTCCCGACC	1200
QY	1273	CCCGACTCTGGGCTGAGTGTGGCGCATGCGCTGCTCCCGCAGCAGATGAGCAGCTC	1332
Db	1201	CCCGACTCTGGGCTGAGTGTGGCGCATGCGCTGCTCCCGCAGCAGATGAGCAGCTC	1260
QY	1333	CTGCACGCGCGGAG	1392
Db	1261	CTGCACGCGCGGAG	1320
QY	1393	CGCTACATTTGCAATTCGCTTCGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG	1452
Db	1321	CGCTACATTTGCAATTCGCTTCGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAG	1380
QY	1453	AAGTTCGCGCGCTGAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1512
Db	1381	AAGTTCGCGCGCTGAGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1440
QY	1513	ATCTGCACCATCGGAG	1572
Db	1441	ATCTGCACCATCGGAG	1500
QY	1573	TTTGGCTAA 1581	
Db	1501	TTTGGCTAA 1509	
RESULT 9			
AAC90385			
ID	AAC90385 standard; cDNA; 1509 BP.		
XX	AAC90385;		
AC	AAC90385;		
DT	14-MAR-2001 (first entry)		
DE	Mutant human alpha7 ligand gated ion channel coding sequence #1.		
KW	Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;		
KW	5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.		
OS	Homo sapiens.		
XX	WO200073431-A2.		
PD	07-DEC-2000.		
PF	25-MAY-2000; 2000WO-US011862.		
PR	27-MAY-1999; 99US-0136174P.		
PA	(PHAA) PHARMACIA & UPJOHN CO.		
PI	Groppi VE, Wolfe ML, Berkenpas MB;		
XX	WPI; 2001-061524/07.		
DR	P-PSDB; AAB50015.		
XX	Special cell culture medium for treating cells and for inducing mammalian		
PT	cell lines to conduct calcium ions, comprising specified concentrations		
PT	of ions of sodium, calcium and potassium at specified pH.		
XX	Claim 50; Page 69; 77pp; English.		

PI Groppi VE, Wolfe ML, Berkenpas MB;
XX WPI; 2001-061524/07.
DR P-PSDB; AAB50016.
XX
XX Special cell culture medium for treating cells and for inducing mammalian
PT cell lines to conduct calcium ions, comprising specified concentrations
PT of ions of sodium, calcium and potassium at specified pH.
XX
XX Claim 57; Page 72; 77pp; English.
XX
XX The present sequence is the coding sequence for a mutant human alpha7
CC nicotinic acetylcholine gated ion channel. The human alpha7 ion channel
CC was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)
CC chimeric ligand gated ion channel (see AAC90382 and AAB50014). The
CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
CC in the present invention, resulting in preferential calcium ion
CC conductance by the cells. The protein encoded by this sequence has the
CC wild-type cysteine residue at position 241 substituted by a serine
CC residue
XX
SQ Sequence 1509 BP; 298 A; 451 C; 429 G; 331 T; 0 U; 0 Other;
Query Match 80.3%; Score 1507; DB 4; Length 1509;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1507; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 73 ATGCGTCTCGCGGGAGGCGTCTGGCTGGCGCTGGCGGCTGCTCTCTGCAAGTGTC 132
Db 1 ATGCGTCTCGCGGGAGGCGTCTGGCTGGCGCTGGCGGCTGCTCTCTGCAAGTGTC 60
Qy 133 CTGCAAGCGGAGTTCAGAGGAGCTTTACAGAGCTGGTCAAGACTCAATCCCTTG 192
Db 61 CTGCAAGCGGAGTTCAGAGGAGCTTTACAGAGCTGGTCAAGACTCAATCCCTTG 120
Qy 193 GAGAGGCGGCTGGCGCAATGACTCGCAACACTCACCGTCTACTTCTCCCTGAGCCTCCTG 252
Db 121 GAGAGGCGGCTGGCGCAATGACTCGCAACACTCACCGTCTACTTCTCCCTGAGCCTCCTG 180
Qy 253 CAGATCATGAGCTGGAGTGAAGAACCAAGTTTAAACCAACCAATTTGGCTGCAATG 312
Db 181 CAGATCATGAGCTGGAGTGAAGAACCAAGTTTAAACCAACCAATTTGGCTGCAATG 240
Qy 313 TCTTGGACAGATCACTATTACAGTGAATGTGTCAGAAATTCAGAGGCTGAAGCTGTT 372
Db 241 TCTTGGACAGATCACTATTACAGTGAATGTGTCAGAAATTCAGAGGCTGAAGCTGTT 300
Qy 373 CGTTTCCAGATGGCCAGATTGGAAACAGACATCTTCTCTATAACAGTGTGATGAG 432
Db 301 CGTTTCCAGATGGCCAGATTGGAAACAGACATCTTCTCTATAACAGTGTGATGAG 360
Qy 433 CGTTTGGACGCAATTCACACTAACCTGTGGTGAATTTCTTGGGCAATGGCCAGTAC 492
Db 361 CGTTTGGACGCAATTCACACTAACCTGTGGTGAATTTCTTGGGCAATGGCCAGTAC 420
Qy 493 CTGCTCCAGGCAATTCAGAGTTCCTGCTACATCGATGACGCTGGTTCCCTTTGAT 552
Db 421 CTGCTCCAGGCAATTCAGAGTTCCTGCTACATCGATGACGCTGGTTCCCTTTGAT 480
Qy 553 GTGACGACTGCAAACTGAAGTTTGGGTCCTGGTCTTACGGAGGCTGGTCTTGGATCTG 612
Db 481 GTGACGACTGCAAACTGAAGTTTGGGTCCTGGTCTTACGGAGGCTGGTCTTGGATCTG 540
Qy 613 CAGATGCAAGGCGAGATATCAGTGGCTATATCCCAATGGAGAACTAGTGGGA 672
Db 541 CAGATGCAAGGCGAGATATCAGTGGCTATATCCCAATGGAGAACTAGTGGGA 600
Qy 673 ATCCCGGCGAGAGAGTGAAGGTTCTATGAGTGTCTGCAAGAGCCCTACCCGATGTC 732
Db 601 ATCCCGGCGAGAGAGTGAAGGTTCTATGAGTGTCTGCAAGAGCCCTACCCGATGTC 660
Qy 733 ACCTTCAGTGAACATCGCGCGGAGGAGCTCTACTATGGCTCAACCTGCTGATCCCG 792

Db 661 ACCTTCAGTGAACCATGCGCCGCGAGGACGCTCTACTATAGCCCTCAACCTGCTGATCCCC 720
Qy 793 TGTGTGCTCATCTCCGCCCTCGCCCTGCTGTGTGTTCTGTCTTCTGAGATTCGGGGAG 852
Db 721 AGTGTGCTCATCTCCGCCCTCGCCCTGCTGTGTGTTCTGTCTTCTGAGATTCGGGGAG 780
Qy 853 AAGATTTCCCTGGGGATAACAGTCTTACTCTCTTACCGCTTTCATGCTGCTGTGCT 912
Db 781 AAGATTTCCCTGGGGATAACAGTCTTACTCTCTCTTACCGCTTTCATGCTGCTGTGCT 840
Qy 913 GAGATCATGCGCGCAACATCCGATTCGGTACCATTTAGTACCCAGTACTTCCGCCAGCAC 972
Db 841 GAGATCATGCGCGCAACATCCGATTCGGTACCATTTAGTACCCAGTACTTCCGCCAGCAC 900
Qy 973 ATGATCATGCTGGGCTCTCGGTGGTGTGACGGTGTGCTGTGCTGACAGTACCAACAC 1032
Db 901 ATGATCATGCTGGGCTCTCGGTGGTGTGACGGTGTGCTGTGCTGACAGTACCAACAC 960
Qy 1033 GACCCGAGCGGGGCAAGATGCCCAAGTGAACCAAGTATCTTCTGAACTGGTGGCG 1092
Db 961 GACCCGAGCGGGGCAAGATGCCCAAGTGAACCAAGTATCTTCTGAACTGGTGGCG 1020
Qy 1093 TGGTTCCTSCGAATGAAGAGGCCCGGGGAGACAAAGTGGCGCGCTGCGCACACAAG 1152
Db 1021 TGGTTCCTSCGAATGAAGAGGCCCGGGGAGACAAAGTGGCGCGCTGCGCACACAAG 1080
Qy 1153 CAGCGGCGCTGCACCTGGCAGTGTGAGATGAGCGCGGTGGCGCGCGCGCGCGCGCG 1212
Db 1081 CAGCGGCGCTGCACCTGGCAGTGTGAGATGAGCGCGGTGGCGCGCGCGCGCGCGCG 1140
Qy 1213 AACGGGAACCTGCTGTATCATCGGCTTCGGCGGCTTGACACGGCGTGTGCTGCTCCGAC 1272
Db 1141 AACGGGAACCTGCTGTATCATCGGCTTCGGCGGCTTGACACGGCGTGTGCTGCTCCGAC 1200
Qy 1273 CCCGACTCTGGGCTAGTGTGGCGCATGTCCTGCTCCCGCACGACGATGACACCTC 1332
Db 1201 CCCGACTCTGGGCTAGTGTGGCGCATGTCCTGCTCCCGCACGACGATGACACCTC 1260
Qy 1333 CTGCAACGCGGCAACCCCGAGGGGACCCGAGCTTGGCAAGATCTCTGGAGAGGTC 1392
Db 1261 CTGCAACGCGGCAACCCCGAGGGGACCCGAGCTTGGCAAGATCTCTGGAGAGGTC 1320
Qy 1393 CGCTACATGTCATTCGTTCCGCTGCGAGCAAGAGCGAGCGGCTGTGAGCGAGTGG 1452
Db 1321 CGCTACATGTCATTCGTTCCGCTGCGAGCAAGAGCGAGCGGCTGTGAGCGAGTGG 1380
Qy 1453 AAGTTTCGCGGCTGTGTGTGACCGCTGTGCTCATGGCTTCTCGGCTCTTCCACCATC 1512
Db 1381 AAGTTTCGCGGCTGTGTGTGACCGCTGTGCTCATGGCTTCTCGGCTCTTCCACCATC 1440
Qy 1513 ATCTGCACCATTCGGCATCTCGATTCGGCTCCCAACTTCGTGGAGGCGGCTGTCCAAAGAC 1572
Db 1441 ATCTGCACCATTCGGCATCTCGATTCGGCTCCCAACTTCGTGGAGGCGGCTGTCCAAAGAC 1500
Qy 1573 TTTTCGGTAA 1581
Db 1501 TTTTCGGTAA 1509
RESULT 11
AAC58395
ID AAC58395 standard; cDNA; 1509 BP.
XX AAC58395;
XX
XX 29-JAN-2001 (first entry)
XX
DE Human PRO2145 nucleotide sequence SEQ ID NO: 76.
XX
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neutrotic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; angiogenic; leukaemia; lymphoid malignancy;

neuronal disorder; glial disorder; astrocytal disorder; angiogenic; hypothalamic disorder; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immunologic disorder; ss.

Homo sapiens.

WO200053755-A2.

14-SEP-2000

06-JAN-2000: 2000WO-US000376.

08-MAR-1999: 99WO-IIS005028.

02-JUN-1999; 99WO-US012252.
23-JUN-1999; 99US-0141037D

07-JUL-1999; 99US-0143048P.
26-JUL-1999; 99US-0145698D

30-NOV-1999; 99WO-US028313.
30 DEC 1999; 99WO US020911

05-JAN-2000; 2000WO-US000219.

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, God

P-PSDB; AAB24088.

Thirty PRO polynucleotides encoding PRO polypeptides, useful in the

readable, unambiguous

Claim 50; Fig 57;

[illegible]

PRO717, PRO809, PRO830, PRO848, F

PRO1281, PRO2023, PRO339, PRO834, PRO1317, PRO1710, PRO20594, PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The PRO polypeptides and nucleotides are useful in the treatment, diagnosis and prevention of cancer. The antibodies and other anti-tumour compounds may be used to treat various conditions, including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoealic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC58362 represent PCR primers and hybridisation probes used in the isolation of the human PRO sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 1509 BP: 297 A: 451 C: 429 G: 332 T: 0 U: 0 Other: 0

Query Match 80.2%; Score 1505.4; DB 3; Length 1509;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1506; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 73 ATGCGCTGCTCGCCGGAGGCCTTGTGGCTGGCGCTGCCGCTCCTCTTGACACGTGTC 132
|||||
Dd 1 ATGCGCTGCTCGCCGGAGGCCTTGTGGCTGGCGCTGCCGCTCCTCTTGACACGTGTC 60

QY 133 CTGCAAGCGAGTTCACAGGAAGCTTTTACAAGGAGCTGGTCAAGAACTAATCCCTTG 192
|||
Db 61 CTGCAAGCGAGTTCACAGGAAGCTTTTACAAGGAGCTGGTCAAGAACTAATCCCTTG 120

Db 1201 CCCGACTCTGGGGTAGTGTGTGGCGCATGTGGCTCTCCGCCACGACGATGAGCACTC 1260
Qy 1333 CTGCAAGCGGGCAACCCCGAGGGGACCCGGACTTTGGCCAAAGATCCTGGAGGAGTC 1392
Db 1261 CTGCAAGCGGGCAACCCCGAGGGGACCCGGACTTTGGCCAAAGATCCTGGAGGAGTC 1320
Qy 1393 CGCTACATTCGCAATCGCTTCGCTGCGCAGGACGAAAGCGAGGCGGTCTGCGAGGAGTGG 1452
Db 1321 CGCTACATTCGCAATCGCTTCGCTGCGCAGGACGAAAGCGAGGCGGTCTGCGAGGAGTGG 1380
Qy 1453 AAGTTCGCGGCTGTGTGGTGGACCGGCTGTGCTCATGGCTTCTCGGTCTTCCACCATC 1512
Db 1381 AAGTTCGCGGCTGTGTGGTGGACCGGCTGTGCTCATGGCTTCTCGGTCTTCCACCATC 1440
Qy 1513 ATCTGCACCATCGGCATCTCTGATGTGCGCTCCCAACTTCGTGGAGGCGGTGTCCAAAGAC 1572
Db 1441 ATCTGCACCATCGGCATCTCTGATGTGCGCTCCCAACTTCGTGGAGGCGGTGTCCAAAGAC 1500
Qy 1573 TTTGCGTAA 1581
Db 1501 TTTGCGTAA 1509

RESULT 12

AAC90387
ID AAC90387 standard; cdna; 1509 BP.
XX
AC AAC90387;
XX
AT 14-MAR-2001 (first entry)
XX
DE Mutant human alpha7 ligand gated ion channel coding sequence #3.
XX
KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
XX
OS Homo sapiens.
XX
FN W0200073431-A2.
XX
PD 07-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US011862.
XX
PR 27-MAY-1999; 99US-0136174P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Groppi VE, Wolfe ML, Berkenpas MB;
XX
DR WPI; 2001-061524/07.
DR P-PSDB; AAB50017.
XX
PT Special cell culture medium for treating cells and for inducing mammalian
PT cell lines to conduct calcium ions, comprising specified concentrations
PT of ions of sodium, calcium and potassium at specified pH.
XX
PS Claim 64; Page 75; 77pp; English.
XX
CC The present sequence is the coding sequence for a mutant human alpha7
CC nicotinic acetylcholine gated ion channel. The human alpha7 ion channel
CC was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)
CC chimeric ligand gated ion channel (see AAC90382 and AAB50014). The
CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
CC in the present invention, resulting in preferential calcium ion
CC conductance by the cells. The protein encoded by this sequence has the
CC wild-type threonine residue at position 230 substituted by a proline
CC residue and the wild-type cysteine residue at position 241 substituted by
XX a serine residue
SQ Sequence 1509 BP; 297 A; 452 C; 429 G; 331 T; 0 U; 0 Other;

Query Match 80.2%; Score 1505.4; DB 4; Length 1509;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1506; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 73 ATGGGCTGCTGCGCGGAGGCGTCTGGCTGGCGCTGGCGGCTGCTCTGCAAGTGTCC 132
Db 1 ATGGGCTGCTGCGCGGAGGCGTCTGGCTGGCGCTGGCGGCTGCTCTGCAAGTGTCC 60
Qy 133 CTGCAAGCGGAGTTCAGAGGAGAGCTTTTACAAGGAGCTGGTCAAGAACTACAATCCCTTG 192
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Db 541 CAGATGAGGAGGAGCAGATATCAGTGGCTATATCCCAATGAGAAATGGGACCTAGTGGGA 600
Qy 673 ATCCCGGCAAGAGGAGTGAAGGTTCTATGAGTGTCTGCAAGAGCCCTACCCCGATGTC 732
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Qy 793 TGTGTGCTCATCTCCGCCCTCGCCCTGCTGCTGCTTCTGCTTCTGAGATTCGCGGAG 852
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Qy 853 AAGATTTCCCTGGGAGTAAACAGTCTTACTCTCTTTACCGCTTTTCATGCTGCTGCTGCT 912
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Db 1081 CAGCGCGCTGAGCGCTGAGCGCGTGGAGATGAGCGCGTGGCGCGCGCGCGCGCG 1140
Qy 1213 AACGGGAACCTGCTGATACATCGCTTCGCGCGCTGGACGGGTGCACTGTGTCCGAC 1272
Db 1141 AACGGGAACCTGCTGATACATCGCTTCGCGCGCTGGACGGGTGCACTGTGTCCGAC 1200
Qy 1273 CCGGACTCTGGGCTAGTGTGGCGCGCATGCGCTGCTCCCGACGACGATGACACCTC 1332
Db 1201 CCGGACTCTGGGCTAGTGTGGCGCGCATGCGCTGCTCCCGACGACGATGACACCTC 1260
Qy 1333 CTGACGGCGGGCAACCCCGAGGGGACCGCGACTTGGCCAAAGATCTCGAGGAGGTC 1392
Db 1261 CTGACGGCGGGCAACCCCGAGGGGACCGCGACTTGGCCAAAGATCTCGAGGAGGTC 1320
Qy 1393 CGCTACATTGCCAATCGCTTCGCTGCCAGGACGAAAGCGAGCGGTCTGCGAGCGAGTG 1452
Db 1321 CGCTACATTGCCAATCGCTTCGCTGCCAGGACGAAAGCGAGCGGTCTGCGAGCGAGTG 1380
Qy 1453 AAGTTGCGCGCTGTGTGGTGGACCGCGCTGTGCTCATGGCTTCTCGGTCTTCAACATC 1512
Db 1381 AAGTTGCGCGCTGTGTGGTGGACCGCGCTGTGCTCATGGCTTCTCGGTCTTCAACATC 1440
Qy 1513 ATCTGACCATCGGATCTGATGTGCGGTCCCAACTTGTGGAGCGCGGTGTCGAAGAC 1572
Db 1441 ATCTGACCATCGGATCTGATGTGCGGTCCCAACTTGTGGAGCGCGGTGTCGAAGAC 1500
Qy 1573 TTTGCGTAA 1581
Db 1501 TTTGCGTAA 1509

RESULT 13

AAS79730
ID AAS79730 standard; cDNA; 2511 BP.
XX
AC AAS79730;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #15534.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSB-) HYSB INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG15543.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 15534; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2511 BP; 523 A; 737 C; 692 G; 559 T; 0 U; 0 Other;
Query Match 68.2%; Score 1279; DB 5; Length 2511;
Best Local Similarity 98.6%; Pred. No. 1e-268;
Matches 1363; Conservative 1; Mismatches 11; Indels 8; Gaps 7;
Qy 500 CAGGCATATTCAGAGTTCTCTGCTACATCGATGATGCTGTTCCCTTTGATGTCAGC 559
Db 964 CAGGCATATTCAGAGTTCTCTGCTACATCGATGATGCTGTTCCCTTTGATGTCAGC 1023
Qy 560 ACTGCAAACTGAAGTTGGTCTCTTACGGAGGTGGTCTTGGATCTGCAGATGC 619
Db 1024 ACTGCAAACTGAAGTTGGTCTCTTACGGAGGTGGTCTTGGATCTGCAGATGC 1083
Qy 620 AGGA-GGCGAGATATC-AGTGGCTATATCCCAATGGAGATGGACCTAGTGGATCCC 677
Db 1084 AGGACGGCAGATATCAAGTGGCTATATCCCAATGGAGATGGACCTAGTGGATCCC 1143
Qy 678 CGGCAAGAGGAGTGAAGGTTCTATGAGTGTCTGCAAGAGCCCTACCCGATGTACCTT 737
Db 1144 CGGCAAGAGGAGTGAAGGTTCTATGAGTGTCTGCAAGAGCCCTACCTGATGTACCTT 1203
Qy 738 CACAGTGCACATGCGCGCAGAGCGCTCTA- -TGGCCTCAACCTGTGTATCCCTGT 795
Db 1204 CACAGTGCACATGCGCGCAGAGCGCTCTA- -TGGCCTCAACCTGTGTATCCCTGT 1263
Qy 796 GTGCTCATCTCGCCCTTCCCT- -GCTGGTGTCTCTGCTTCTGAGATTCGGGAGAA 854
Db 1264 GTGCTCATCTCGCCCTTCCCTGCTGGTGTCTCTGCTTCTGAGATTCGGGAGAA 1323
Qy 855 GATTTCCCTCGGGATAAACAGTCTTACTCTCTCTTACCGTCTTCTATGCTGCTGCTGA 914
Db 1324 GATTTCCCTCGGGATAAACAGTCTTACTCTCTCTTACCGTCTTCTATGCTGCTGA 1383
Qy 915 GATCATGCGCGCAACATCCGATTCGCTACATGATAGCCAGTACTTCCGACGACCAT 974
Db 1384 GATCATGCGCGCAACATCCGATTCGCTACATGATAGCCAGTACTTCCGACGACCAT 1443
Qy 975 GATCATGCGCGCTCTCGTGTGTGACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1034
Db 1444 GATCATGCGCGCTCTCGTGTGTGACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1503
Qy 1035 CCGGACGGGGCAGATGCCCAAGTGGACAGAGTCACTTCTTGAATGGTGGCGGTG 1094
Db 1504 CCGGACGGGGCAGATGCCCAAGTGGACAGAGTCACTTCTTGAATGGTGGCGGTG 1563
Qy 1095 GTTCTCTGAAATGAAGAGCGCGGGAGGAGAGAGTGGCGCGCGCTGCGAGCAAGCA 1154
Db 1564 GTTCTCTGAAATGAAGAGCGCGGGAGGAGAGTGGCGCGCGCTGCGAGCAAGCA 1623


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Qy 373 CGTTTCCAGATGGCCAGATTGGAAACACAGACATTTCTCTATACAGTGTGATGAG 432
Db |||||
Qy 301 CGTTTCCAGATGGCCAGATTGGAAACACAGACATTTCTCTATACAGTGTGATGAG 360
Db |||||
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Job time : 796 secs

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OM nucleic - nucleic search, using sw model

Run on: May 8, 2004, 15:51:58 ; Search time 7438 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 34: em_hg_pln.*
- 35: em_hg_tod.*
- 36: em_hg_nam.*
- 37: em_hg_vrt.*
- 38: em_sy.*
- 39: em_hgo_hum.*
- 40: em_hgo_mus.*
- 41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1875.6	100.0	1876	6	AR055255	AR055255 Sequence
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3	1875.6	100.0	1876	6	AR173187	AR173187 Sequence
4	1875.6	100.0	1876	6	AR224030	AR224030 Sequence
5	1875.6	100.0	1876	6	AR282833	AR282833 Sequence
6	1875.6	100.0	1876	6	AX719088	AX719088 Sequence
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8	1801.2	96.0	1916	9	AF385585	AF385585 Homo sapi
9	1801	96.0	1977	9	HSU40583	U40583 Human alpha
10	1801	96.0	2087	9	HSARA7A	X70297 H.sapiens m
11	1745.2	93.0	2107	9	AF486623	AF486623 Macaca mu
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14	1520.4	81.0	1559	9	HUMA7NAR	L25827 Human a7 ni
15	1508.6	80.4	1509	6	AX054567	AX054567 Sequence
16	1507	80.3	1509	6	AX054575	AX054575 Sequence
17	1507	80.3	1509	6	AX054577	AX054577 Sequence
18	1505.4	80.2	1509	6	AX054579	AX054579 Sequence
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23	1391.2	74.2	1712	9	AF036903	AF036903 Homo sapi
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28	1197.4	63.8	3030	10	SS3987	X93604 B.taurus mR
29	966	51.5	2037	5	GGNARA7A	SS3987 nicotinic r
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ALIGNMENTS

RESULT 1
AR055255

LOCUS

AR055255

DEFINITION

Sequence 7 from patent US 5837489.

ACCESSION

AR055255

VERSION

AR055255.1 GI:5980832

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 1876)

AUTHORS

Elliot, K.J., Ellis, S.B. and Harpold, M.M.

TITLE

Human neuronal nicotinic acetylcholine receptor and cells

JOURNAL

transformed with same DNA and mRNA encoding an--subunit of

Patent: US 5837489-A 7 17-NOV-1998;

linear DNA 1876 bp PAT 29-SEP-1999

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		/mol_type="unassigned DNA"
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Best Local Similarity		100.0%; Pred. No. 0;
Matches 1876; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
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DB	1	GGCCGAGCGGCGAGCGCGGCGGCGAGCGGAGACGCTGGAGCGCGCGCGCTGCGTGCAGCT 60
QY	61	CGGGGACTCAACATGCGCTGCTCGCGGAGGCGCTGCTGCTGCGCTGCGCTGCGCTGCGCTC 120
DB	61	CGGGGACTCAACATGCGCTGCTCGCGGAGGCGCTGCTGCTGCGCTGCGCTGCGCTGCGCTC 120
QY	121	CTGACGCTGCTCCGCAAGGCGAGTTCAGAGGAAGCTTTCAAGGAGCTGGTCAAGAAC 180
DB	121	CTGACGCTGCTCCGCAAGGCGAGTTCAGAGGAAGCTTTCAAGGAGCTGGTCAAGAAC 180
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DB	181	TACATCCCTTGAGAGGCGCGTGGCCATGACTCGGAACCACTCACCGTCTACTTCTCC 240
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DB	241	CTGAGCTCTGCGAGATCATGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY	301	TGGCTGAAATGCTTGGACAGATCACTATTTCAGTGGAAATGTGTCAGAAATATCCAGGG 360
DB	301	TGGCTGAAATGCTTGGACAGATCACTATTTCAGTGGAAATGTGTCAGAAATATCCAGGG 360
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DB	361	GTGAAGACTGCTTGGACAGATCACTATTTCAGTGGAAATGTGTCAGAAATATCCAGGG 420
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QY	1321	GATGAGCACTCTCTGCAACGCGGCGGCAACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
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QY	1381	CTGAGGAGGCTCGCTTACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
DB	1381	CTGAGGAGGCTCGCTTACATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
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DB	1441	TGCGAGGAGTGGAGGTTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
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QY	1561	GTGTCCAAAGACTTTCGCTTAAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
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RESULT 2

AR071403

LOCUS

DEFINITION

AR071403

ACCESSION

AR071403.1

VERSION

KEYWORDS

Sequence 7 from patent US 5910582.

1876 bp

DNA

linear

PAT 18-FEB-2000

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1876)
AUTHORS Elliott,K.J., Ellis,S.B. and Harpold,M.M.
TITLE Human neuronal nicotinic acetylcholine receptor compositions and methods employing same
JOURNAL Patent: US 5910582-A 7 08-JUN-1999;
FEATURES Location/Qualifiers
source 1..1876
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 1875.6; DB 6; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||

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RESULT 3
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LOCUS ARI173187 1876 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 7 from patent US 6303753.
ACCESSION ARI173187
VERSION ARI173187.1 GI:17912678
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1. (bases 1 to 1876)
ELLIOTT,K.J., ELLIS,S.B. and HARPOLD,M.M.
TITLE Human neuronal nicotinic acetylcholine receptor compositions and
methods employing same
JOURNAL Patent: US 6303753-A 7 16-OCT-2001;
FEATURES
source Location/Qualifiers
1..1876
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ORIGIN
Query Match 100.0%; Score 1875.6; DB 6; Length 1876;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 11 from patent US 6524789.
ACCESSION AR282833
VERSION AR282833.1 GI:29719625
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 1876)
Elliott, K.J. and Harpold, M.M.
Human neuronal nicotinic acetylcholine receptor compositions and

TITLE

methods employing same
Patent: US 6524789-A 11 25-FEB-2003;

JOURNAL

Location/Qualifiers

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RESULT 7
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LOCUS Human nicotinic acetylcholine receptor alpha7 subunit precursor,
DEFINITION mRNA, complete cds.
ACCESSION U62436
VERSION U62436.1 GI:1458119
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1876)
AUTHORS Elliott,K.J., Ellis,S.B., Berckhan,K.J., Urrutia,A.,
Chavez-Noriega,L.E., Johnson,E.C., Velicelebi,G. and Harpold,M.M.
TITLE Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
beta 4 subunits

J. Mol. Neurosci. 7 (3), 217-228 (1996)
97062879
8906617
PUBMED
REFERENCE 2 (bases 1 to 1876)
AUTHORS Elliott,K.J.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1996) Kathryn J. Elliott, SIBIA Neurosciences,
Inc., 505 Coast Blvd. So., La Jolla, CA 92037, USA
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Query Match 100.0%; Score 1875.6; DB 9; Length 1876;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1875; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 alpha-7 subunit.
 X70297
 ACCESSION X70297.1 GI:496606
 VERSION neuronal nicotinic acetylcholine receptor alpha-7 subunit.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Peng, X., Katz, M., Gerzanich, V., Anand, R. and Lindstrom, J.
 TITLE Human alpha 7 acetylcholine receptor: cloning of the alpha 7
 subunit from the SH-SY5y cell line and determination of
 pharmacological properties of native receptors and functional alpha
 7 homomers expressed in Xenopus oocytes
 Mol. Pharmacol. 45 (3), 546-554 (1994)

JOURNAL 94195283
 MEDLINE 8145738
 PUMED 2 (bases 1 to 2087)
 REFERENCE
 AUTHORS Katz, M.
 TITLE Direct Submission
 JOURNAL Submitted (04-FEB-1993) M. Katz, Univ of Pennsylvania School of
 Medicine, Dept of Neuroscience, 36th & Hamilton Walk, Rm 235
 Stemmler Hall, Philadelphia, PA 19104, USA

FEATURES

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RESULT 11
AF486623
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DEFINITION
Macaca mulatta nicotinic acetylcholine receptor alpha7 (CHRNA7)
mRNA, complete cds.
AF486623
ACCESSION

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

gene
5' UTR
CDS

3' UTR

ORIGIN

Query Match 93.0%; Score 1745.2; DB 9; Length 2107;
Best Local Similarity 95.9%; Pred. No. 2.2e-307;
Matches 1800; Conservative 1; Mismatches 74; Indels 1; Gaps 1;

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AF486623.1 GI:29422147

Macaca mulatta (rhesus monkey)
Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.

1 (bases 1 to 2107)

Proskocil, B.J., Sekhon, H.S., Kellier, J.A., Jia, Y., Blakely, R.D.,
Lindstrom, J., and Spindel, E.R.
An Intrinsic Non-neuronal Nicotinic Cholinergic Signaling System in
Monkey Lung Airway Epithelium

2 (bases 1 to 2107)

Proskocil, B.J., Sekhon, H.S., Kellier, J.A., Jia, Y., Blakely, R.D.,
Lindstrom, J., and Spindel, E.R.

Direct Submission

Submitted (21-FEB-2002) Neuroscience, Oregon Regional Primate

Research Center, 505 NW 185th Ave., Beaverton, OR 97006, USA

Location/Qualifiers

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VERSION AR261850.1 GI:28073040
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ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1590)
AUTHORS Briggs,C.A., Gopalakrishnan,M., McKenna,D.G., Monteggia,L.M.,
Roch,J.-M., Sullivan,J.P. and Touma,E.
TITLE Variant human .alpha.7 acetylcholine receptor subunit, and methods
of production and uses thereof
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QY	1272	CCCCGACTCTGGGGTAGTGTGTGGCCGATGGCCTGTCTCCCCACGCAACGATGAGCACT	1331
Db	1208	CCCCGACTCTGGGGTAGTGTGTGGCCGATGGCCTGTCTCCCCACGCAACGATGAGCACT	1267
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[illegible]

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LOCUS 1559 bp mRNA linear PRI 04-JAN-1994
DEFINITION Human a7 nicotinic acetylcholine receptor mRNA.
ACCESSION L25827
VERSION L25827.1 GI:438616
KEYWORDS nicotinic acetylcholine receptor alpha 7 subunit; transmembrane protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Doveitte-Stamm, L., Monteggia, L.M., Donnelly-Roberts, D., Wang, M.T., Lee, J., Tian, J. and Giordano, T.
TITLE Cloning and sequence of the human a7 nicotinic acetylcholine receptor
JOURNAL Drug Dev. Res. (1993) In press
COMMENT Original source text: Homo sapiens (library: Clontech HL1065b; ATCC 37433) fetus brain cDNA to mRNA.
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Query Match 81.0%; Score 1520.4; DB 9; Length 1559;
Best Local Similarity 99.5%; Pred. No. 1.7e-266;
Matches 1524; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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AX054567
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DEFINITION Sequence 1 from Patent WO0073431.
ACCESSION AX054567
VERSION AX054567.1 GI:12228147
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
Groppi, V. E., Wolfe, M. L. and Berkenpas, M. B.
METHODS AND COMPOSITIONS FOR MEASURING ION CHANNEL CONDUCTANCE
PATENT: WO 0073431-A 1 07-DEC-2000;
PHARMACIA & UPJOHN COMPANY (US)
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Query Match 80.4%; Score 1508.6; DB 6; Length 1509;
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QY 133 CTGCAAGCGGAGTTCAGAGGAGCTTTACAGAGGCTGTGTCAGAGTCAATCCCTTG 192
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